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XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Kadnick KS, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX WPI; 2001-536566/59.
DR N-PSDB; AAD16347.
XX
PT New secreted and membrane associated polypeptides for treating
PT Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
PT disorders, stroke, and asthma -
XX
PS Claim 1; Page 58-59; 94pp; English.
XX
CC The present sequence is a human sbhgcta protein,
CC a secreted protein of the invention.
CC The invention relates to secreted and membrane associated polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating diseases such as Alzheimer's disease,
CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
CC of the immune system, hematopoietic disease, inflammation, anxiety,
CC schizophrenia, feeding disorders, anorexia, depression, social, sexual
CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning
CC and memory alteration and altered immune response, seizure, migraine,
CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
CC of transsexuals, growth abnormalities, obesity, infections, autoimmune
CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
CC disorders associated with healthy maintenance of gastric mucosa and
CC repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
CC amaemia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,
CC viral and non-viral hepatitis, type I and type II diabetes mellitus,
CC glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
CC paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
CC invention are used to identify membrane bound and soluble receptors.
CC They are also useful as vaccines for inducing an immunological response
CC in a mammal. Polynucleotides of the invention are used in gene therapy.
CC They are also valuable for chromosome localisation studies and tissue
CC expression studies.
XX
SQ Sequence 130 AA;
Query Match 100.0%; Score 722; DB 22; Length 130;
Best Local Similarity 100.0%; Pred. No. 9,1e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAEFLGPMALLLAGYGVLAGSSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
DB 1 mklaefllgpmallllagygcvlgsasgnlrtfvgcavrefflakpgcgrlrlttddc 60
QY 61 WGRCTEWKPILEPPYIEAHHRVCTYNETKQYTVKLPNCAGVDPFYTYPAVAIRDCGAC 120
DB 61 wgrctewkpiileppyieahhrvctyneckytklpncapgvdpfytypvairdcgac 120
QY 121 STATTECETI 130
DB 121 stattececi 130
RESULT 2
AAG63211
ID AAG63211 standard; Protein; 130 AA.
XX
AC AAG63211;
XX
DT 01-OCT-2001 (first entry)
XX
DE Amino acid sequence of a human cystine knot polypeptide.
XX
KW Cystine knot polypeptide; follicular arrest; recruitment modulator;
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KW fertility-related disorder; contraception; menopause; contraceptive;
KW follicle growth.
XX
OS Homo sapiens.
XX
PN WO200153346-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-EP00570.
XX
PR 18-JAN-2000; 2000EP-0200185.
XX
PA (ALKU ) AKZO NOBEL NV.
XX
PI Mosselman S, Spek Van Der Pij;
XX
XX WPI; 2001-476102/51.
XX
DR N-PSDB; AAH42567.
XX
PT New DNA sequences, useful for coding or producing cystine knot
PT polypeptides, which are useful in preparing a pharmaceutical for
PT fertility-related disorders or contraception, and for controlling
PT follicular arrest and recruitment -
XX
PS Example 1; Page 23-24; 29pp; English.
XX
CC The present sequence represents a human cystine knot polypeptide. The
CC polypeptide is a follicular arrest and recruitment modulator. Cystine
CC knot polypeptides are useful in preparing a pharmaceutical for
CC fertility-related disorders or in contraception. The polypeptide is
CC particularly useful for controlling follicular arrest and recruitment.
CC Inhibition of recruitment can be used to delay (premature) menopause or
CC as a contraceptive. The polypeptide is also useful for in vitro
CC maturation and growth of follicles, e.g. from frozen ovarian tissue.
XX
SQ Sequence 130 AA;
Query Match 100.0%; Score 722; DB 22; Length 130;
Best Local Similarity 100.0%; Pred. No. 9,1e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAEFLGPMALLLAGYGVLAGSSGNLRTFVGCAVREFTFLAKKPGCGRLRTTDDAC 60
DB 1 mklaefllgpmallllagygcvlgsasgnlrtfvgcavrefflakpgcgrlrlttddc 60
QY 61 WGRCTEWKPILEPPYIEAHHRVCTYNETKQYTVKLPNCAGVDPFYTYPAVAIRDCGAC 120
DB 61 wgrctewkpiileppyieahhrvctyneckytklpncapgvdpfytypvairdcgac 120
QY 121 STATTECETI 130
DB 121 stattececi 130
RESULT 3
AAG64064
ID AAG64064 standard; protein; 130 AA.
XX
AC AAG64064;
XX
DT 17-SEP-2001 (first entry)
XX
DE Human anterior pituitary hormone-related polypeptide.
XX
KW Human; anterior pituitary hormone; hypertension; autoimmune disease;
XX heart failure.
XX
OS Homo sapiens.
XX
KW WO200144475-A1.
XX
PN
```

PD 21-JUN-2001.  
XX  
XX 15-DEC-2000; 2000WO-JP08986.  
XX  
XX 17-DEC-1999; 99JP-0358707.  
PR 18-FEB-2000; 2000JP-0046825.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Hinuma S, Fukusumi S, Fujii R, Hosoya M;  
XX  
DR WPI; 2001-408485/43.  
DR N-PSDB; AAH46586.  
XX  
XX Polypeptides for treatment of hypertension, autoimmune disease and  
PT heart failure -  
XX  
PS Claim 1; Fig 2; 107pp; Japanese.  
XX  
XX The invention relates to a novel polypeptide comprising a fully defined  
CC 130 amino acid sequence given in the specification and its amides,  
CC esters and salts. The polypeptide has anterior pituitary hormone-related  
CC activity. It is useful for the treatment of hypertension, autoimmune  
CC diseases and heart failure. The screening method and kit also  
CC provided in the invention are useful for identifying new substances  
CC for treating and preventing these diseases. The present sequence is  
CC the polypeptide of the invention.  
XX  
SQ Sequence 130 AA;

Query Match 100.0%; Score 722; DB 22; Length 130;  
Best Local Similarity 100.0%; Pred. No. 9, 1e-70;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAFLFLGPMALLLAGYGCYLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRTTDDAC 60  
Db 1 mklafllfipmalllllagycvlgassgnlrtlftvgcavreflflakkgpcrglrlttddac 60  
QY 61 WGRCEWEKPTLEPPYIEAHHRVCTYNETKQVYTKLPNCARGVDPFTTYPRATCDGAC 120  
Db 61 wgrcetwekptleppyleahhrvctyneckqvtklpncapgvdpftlypvalrctdcgac 120  
QY 121 STATTECETI 130  
Db 121 stattecti 130

RESULT 4  
AAB84998  
ID AAB84998 standard; Protein; 230 AA.  
XX  
XX AAB84998;  
XX  
XX 06-AUG-2001 (first entry)  
XX  
XX Human novel gonadotropin (NOVGON) protein.  
XX  
XX NOVG; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;  
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;  
KW cytosolic; neuroprotective; reproductive; antiinflammatory; cancer;  
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;  
KW antiallergic; antiallergic.  
XX  
XX Homo sapiens.  
XX  
XX WO200140291-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 06-DEC-2000; 2000WO-US303029.  
XX  
XX 06-DEC-1999; 99US-0169056.  
PR

PR 09-DEC-1999; 99US-0169866.  
PR 09-DEC-1999; 99US-0169886.  
PR 10-DEC-1999; 99US-0170252.  
PR 12-JAN-2000; 2000US-0175740.  
PR 03-DEC-2000; 2000US-0170252.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zernhusen BD;  
PI Mezes PS;  
XX  
DR WPI; 2001-374790/39.  
DR N-PSDB; AAF83867.  
XX  
XX Novel isolated human transmembrane, neuromedin peptide  
PT gonadotropin-like protein and interleukin-1 receptor antagonist  
PT proteins, useful for treating cancer, immune response disorder,  
PT metabolic function disorders -  
XX  
XX  
PS Claim 1; Fig 6B; 138pp; English.

CC The invention provides novel polypeptides (NOVG) selected from human  
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),  
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor  
CC antagonist proteins (NOVINTRA A and B). The invention also provides  
CC methods in which a NOVG polypeptide, polynucleotide and antibody are  
CC used in the detection, prevention and treatment of a broad range of  
CC pathological states. NOVTRAN can be used to treat is a cell signaling  
CC disorder such as cancer, immune response disorder, hematopoietic  
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat  
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of  
CC central nervous system, breast, colon, ovary, kidney, prostate and  
CC thyroid. NOVGON can be used to treat reproductive development disorder,  
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used  
CC to treat bone metabolism or structure disorder, inflammatory response  
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,  
CC arthritis and cancer. The present sequence represents the NOVGON  
CC polypeptide.  
XX  
SQ Sequence 230 AA;

Query Match 96.8%; Score 699; DB 22; Length 230;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-67;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAFLFLGPMALLLAGYGCYLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRTTDDAC 60  
Db 1 mklafllfipmalllllagycvlgassgnlrtlftvgcavreflflakkgpcrglrlttddac 60  
QY 61 WGRCEWEKPTLEPPYIEAHHRVCTYNETKQVYTKLPNCARGVDPFTTYPRATCDGAC 120  
Db 61 wgrcetwekptleppyleahhrvctyneckqvtklpncapgvdpftlypvalrctdcgac 120  
QY 121 STATTE 126  
Db 121 statte 126

RESULT 5  
AAG64067  
ID AAG64067 standard; Protein; 129 AA.  
XX  
XX AAG64067;  
XX  
XX 17-SEP-2001 (first entry)  
XX  
XX Rat anterior pituitary hormone-related polypeptide #1.  
XX  
XX DE Rat; anterior pituitary hormone; hypertension; autoimmune disease;  
KW heart failure.  
XX  
XX Ratus sp.  
OS

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XX MO200144475-A1.
PN
XX
XX 21-JUN-2001.
PD
XX
XX 15-DEC-2000; 2000WO-JP08896.
PE
XX 17-DEC-1999; 99JP-0358707.
PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
PI Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX
XX WPI; 2001-408485/43.
DR N-PSDB; AAH46593.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
XX Claim 2; Page 102-103; 107pp; Japanese.
PS
XX The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence is
CC is a polypeptide provided in the specification.
XX
XX Sequence 129 AA:
SQ
Query Match 85.2%; Score 615.5; DB 22; Length 129;
Best Local Similarity 85.4%; Pred. No. 2.4e-58;
Matches 111; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
QY 1 MKIAFLFLGPMALLLAGYGVLAGSSGNLRFFVGCANREFTFLAKKPGRCGLRITTDAC 60
DB 1 mklvlylvlg-taalllgdsdsvlsssgnlhfcgavreflrvakkgpcrglrittdac 59
QY 61 WGRCEIWEKPIIEPPYIEAHHRVCYINETKQYTKLPNCAPGVDPFYTPVAIRDCGAC 120
DB 60 wgrcetwexkplieppyieahhrvcylnetkrlrvtklpcapgvdpfitypmaivrcdcgac 119
QY 121 STATTECEI 130
DB 120 stattececi 129
RESULT 6
AAG64065
ID AAG64065 standard; Protein; 106 AA.
XX
XX AAG64065;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Human anterior pituitary hormone-related polypeptide #2.
DE
XX Human; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.
XX
XX Homo sapiens.
OS
XX WO200144475-A1.
PN
XX 21-JUN-2001.
PD
XX 15-DEC-2000; 2000WO-JP08896.
PF
XX 17-DEC-1999; 99JP-0358707.
PR
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PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX
XX WPI; 2001-408485/43.
DR N-PSDB; AAH46589.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
XX Claim 3; Page 100; 107pp; Japanese.
PS
XX The invention relates to a novel polypeptide comprising a fully defined
CC 130 amino acid sequence given in the specification and its amides,
CC esters and salts. The polypeptide has anterior pituitary hormone-related
CC activity. It is useful for the treatment of hypertension, autoimmune
CC diseases and heart failure. The screening method and kit also
CC provided in the invention are useful for identifying new substances
CC for treating and preventing these diseases. The present sequence is
CC is a polypeptide of the invention.
XX
XX Sequence 106 AA:
SQ
Query Match 83.1%; Score 600; DB 22; Length 106;
Best Local Similarity 100.0%; Pred. No. 9e-57;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 ASSGNLRFFVGCANREFTFLAKKPGRCGLRITTDACWGRCEIWEKPIIEPPYIEAHHRVC 84
DB 1 assgnlrffvgcavreflrvakkgpcrglrittdacwgrcetwexkplieppyieahhrvc 60
QY 85 TYNETKQYTKLPNCAPGVDPFYTPVAIRDCGACSTATTECEI 130
DB 61 tynektqytklpcapgvdpfitypvaivrcdcgacstattececi 106
RESULT 7
AAG64068
ID AAG64068 standard; Protein; 106 AA.
XX
XX AAG64068;
AC
XX
XX 17-SEP-2001 (first entry)
DT
XX
XX Rat anterior pituitary hormone-related polypeptide #2.
DE
XX Rat; anterior pituitary hormone; hypertension; autoimmune disease;
KW heart failure.
XX
XX Rattus sp.
OS
XX WO200144475-A1.
PN
XX 21-JUN-2001.
PD
XX 15-DEC-2000; 2000WO-JP08896.
PE
XX 17-DEC-1999; 99JP-0358707.
PR 18-FEB-2000; 2000JP-0046825.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Hinuma S, Fukusumi S, Fujii R, Hosoya M;
XX
XX WPI; 2001-408485/43.
DR N-PSDB; AAH46594.
XX
XX Polypeptides for treatment of hypertension, autoimmune disease and
PT heart failure -
XX
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PS Claim 4; Page 104; 107pp; Japanese.  
 XX  
 CC The invention relates to a novel polypeptide comprising a fully defined  
 CC 130 amino acid sequence given in the specification and its amides,  
 CC esters and salts. The polypeptide has anterior pituitary hormone-related  
 CC activity. It is useful for the treatment of hypertension, autoimmune  
 CC diseases and heart failure. The screening method and kit also  
 CC provided in the invention are useful for identifying new substances  
 CC for treating and preventing these diseases. The present sequence is  
 CC is a polypeptide provided in the specification.  
 XX  
 SO Sequence 106 AA;  
 Query Match 79.2%; Score 572; DB 22; Length 106;  
 Best Local Similarity 92.5%; Pred. No. 9.1e-54;  
 Matches 98; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
 QY 25 ASSGNLRTFVGCAYREFTFLAKKPGCGRLRTTDCACGRCETWEKPILEPPYIEAHNRVC 84  
 DB 1 sssgnlhtfvgcayreflvaakpgcrglrittdacwgcetwekpllepyieayhrvc 60  
 QY 85 TYNETKQVTVLPCNAPGVDPFYTTPVAIRDCGACSTRATECETI 130  
 DB 61 tynekrvtvklnpncapgvdpfytpmavrcdcgacstrateceti 106  
 RESULT 8  
 AAG63212  
 ID AAG63212 standard; Protein; 75 AA.  
 XX  
 AC AAG63212;  
 XX  
 DT 01-Oct-2001 (first entry)  
 XX  
 DE Amino acid sequence of human cystine knot polypeptide splice variant.  
 DE  
 KW Cystine knot polypeptide; follicular arrest; recruitment modulator;  
 KW fertility-related disorder; contraception; menopause; contraceptive;  
 KW follicle growth.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153346-A1.  
 PD  
 XX 26-JUL-2001.  
 PF 17-JAN-2001; 2001WO-EP00570.  
 XX  
 PR 18-JAN-2000; 2000EP-0200185.  
 XX  
 PA (ALKU ) AKZO NOBEL NV.  
 XX  
 PI Mosseelman S, Spek Van Der PJ;  
 XX  
 DR WPI: 2001-476102/51.  
 DR N-PSDB; AAH42568.  
 XX  
 PT New DNA sequences, useful for coding or producing cystine knot  
 PT polypeptides, which are useful in preparing a pharmaceutical for  
 PT fertility-related disorders or contraception, and for controlling  
 PT follicular arrest and recruitment -  
 XX  
 PS Example 1; Page 25; 29pp; English.  
 XX  
 CC The present sequence represents a human cystine knot polypeptide splice  
 CC variant. The polypeptide is a follicular arrest and recruitment  
 CC modulator. Cystine knot polypeptides are useful in preparing a  
 CC pharmaceutical for fertility-related disorders or in contraception.  
 CC The polypeptide is particularly useful for controlling follicular  
 CC arrest and recruitment. Inhibition of recruitment can be used to delay  
 CC (premature) menopause or as a contraceptive. The polypeptide is also  
 CC useful for in vitro maturation and growth of follicles, e.g. from

CC frozen ovarian tissue.  
 XX  
 SO Sequence 75 AA;  
 Query Match 51.2%; Score 370; DB 22; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 3e-32;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLAEFLFGPVALLLAGYGVLAGASSGNLRTFVGCAYREFTFLAKKPGCGRLRTTDCAC 60  
 DB 1 mklaeflfgpvalllagycvlgassgnlritvgaavretflakpvcrglrittdac 60  
 QY 61 WGRCEWE 68  
 DB 61 wgrcetwe 68  
 RESULT 9  
 AAB71792  
 ID AAB71792 standard; Protein; 141 AA.  
 XX  
 AC AAB71792;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Bovine luteotropin beta-chain precursor.  
 DE  
 KW Bovine; luteotropin; beta-human chorionic gonadotropin; beta-hCG; anti-HIV;  
 KW cytostatic; antianaemic; vascular; osteopathic; antiinflammatory;  
 KW gene therapy; maternin; MA peptide; pMA peptide;  
 KW human immunodeficiency virus; HIV; cancer; wasting disorder;  
 KW haematopoietic disorder; inflammation; angiogenic disorder.  
 XX  
 OS Bos SP.  
 XX  
 PN WO200110907-A2.  
 PD  
 XX 15-FEB-2001.  
 PF 05-AUG-2000; 2000WO-US21495.  
 XX  
 PR 06-AUG-1999; 99US-0147825.  
 PR 13-MAR-2000; 2000US-0188777.  
 XX  
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.  
 XX  
 PI Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;  
 PI Foulke J, Lewis G;  
 XX  
 DR WPI: 2001-147510/15.  
 XX  
 PT Cells that produce therapeutic beta-human chorionic gonadotropin  
 PT fragments, useful for the treatment of human immunodeficiency virus  
 PT infections, cancers, wasting disorders, hematopoietic disorders,  
 PT inflammation and angiogenic disorders -  
 XX  
 PS Disclosure; Page 26; 185pp; English.  
 XX  
 CC The present sequence is given in a specification relating to  
 CC therapeutic polypeptides originally isolated from human early pregnancy  
 CC urine, now synthetically produced, as well as functional equivalents of  
 CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)  
 CC fragments, designated Maternin (RTM) and referred to as MA and pMA  
 CC peptides, are disclosed. Both native and synthetic MA inhibited growth  
 CC of human tumour cells implanted into immuno-deficient mice by between 60  
 CC to 100%, relative to control studies. The therapeutic MA polypeptides  
 CC may be used for the prevention and treatment of a range of diseases and  
 CC disorders, including human immunodeficiency virus (HIV) infections,  
 CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic  
 CC disorders (e.g. anemias, radiation mediated bone marrow damage and  
 CC trauma related blood loss), inflammation and angiogenic disorders.  
 XX



Db 61 -kepvfkspstvyqhvctyrdvyeitrlpdcppwvdphtvvalscdscloimtd 119  
 OY 127 C 127  
 Db 120 c 120

RESULT 12  
 AAR15106  
 ID AAR15106 standard; Protein: 145 AA.

AC AAR15106:  
 XX 11-FEB-1992 (first entry)  
 DT hCG/BLH chimera, D10.  
 DE hCG/BLH chimera, D10.  
 XX glycoprotein hormone; immuno-castration;  
 KW immuno-contragestive; vaccine; human chorionic gonadotropin;  
 KM luteinising hormone; LH; CG; bovine.  
 OS Homo sapiens.  
 OS Bos taurus.  
 OS WO9116922-A.  
 PN 14-NOV-1991.  
 PD 07-MAY-1991; 91WO-0503162.  
 PE 08-MAY-1990; 90US-0520703.  
 PR (UYNE-) UNIV MED NEW JERSEY.  
 PA Campbell RK, Moyle WR;  
 PI WPI; 1991-353528/48.  
 DR

PT Now glyco-protein hormone analogues - for inducing fertility as  
 PT immuno-castration agents, for suppressing reproductive system  
 PT development and as immuno-contragestive vaccines.  
 PS Table IV; Page 63; 94pp; English.

CC The sequence is an analogue of mature hCG beta subunit having  
 CC several residues replaced by the corresponding residues in the  
 CC bovine LH protein. The chimeric hormone may be useful for identify-  
 CC ing residues which are important for binding to the human receptor  
 CC and may also have applications as an immunogen, agonist and/or  
 CC antagonist.  
 CC See AAR15043, AAR15061-R15125 and AAR15161-R15198.  
 CC XX

SQ Sequence 145 AA;

Query Match 27.3%; Score 197; DB 12; Length 145;  
 Best Local Similarity 39.0%; Pred. No. 2.4e-13;  
 Matches 41; Conservative 18; Mismatches 38; Indels 8; Gaps 4;

OY 26 SSGNLRFFVGCAVREFFLAKKPGCR-GLRITTDACWGRCETWEK--PILPPYIEAHNR 82  
 Db 1 srqplrlp--cqpinalaekacpvcitftscagycpsmkrvlpvllpmpq---r 55  
 OY 83 VCTYNEKQVTVKLPNCAPGVDPFTYVPAIRCDGACSTATTTC 127  
 Db 56 vctylhelrfasvrlpgcpvydpmvstfpvalschgcgpcrlstdc 100

RESULT 13  
 AAM47027  
 ID AAM47027 standard; protein: 131 AA.  
 XX

AC AAM47027;  
 XX 11-MAY-1998 (first entry)  
 DT

DE eCG hormone beta-subunit variant (1-131 amino acid residues).  
 XX Equine; chorionic gonadotropin; hormone; eCG; beta-subunit; treatment;  
 KW follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;  
 KM ovarian disease; variant.  
 OS Family Equidae.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /note= "signal peptide"  
 FT 21..131  
 FT Protein /note= "mature protein"

PN JPI0036399-A.  
 PD 10-FEB-1998.  
 PE 24-JUL-1996; 96JP-0212197.  
 PR 24-JUL-1996; 96JP-0212197.  
 PA (ELED) DENKI KAGAKU KOGYO KK.  
 PI WPI; 1998-174916/16.  
 DR

PT Recombinant truncated equine chorionic gonadotropin hormone - has  
 PT enhanced follicle-stimulating hormone activity and reduced  
 PT luteinising hormone activity; useful as ovulation inducer  
 PS Claim 7; Page -: 16pp; Japanese.

CC This is a variant of the beta-subunit of an equine chorionic gonadotropin  
 CC (eCG) hormone. The variants are created by removing 39 or lesser amino  
 CC acid residues from the C-terminal peptide region of the beta-subunit. The  
 CC recombinant eCG hormone is composed of alpha-subunit and the variant  
 CC beta-subunits of eCG hormone and has a substantially enhanced follicle-  
 CC stimulating hormone (FSH) activity and reduced luteinising hormone (LH)  
 CC activity. The hormone is an ovulation inducer and can be used as an  
 CC agent for the treatment of ovarian diseases.  
 CC Note: This sequence does not appear in the specification. It has been  
 CC created by modifying the eCG beta-subunit sequence provided in Page 11.  
 CC XX

SQ Sequence 131 AA;

Query Match 25.4%; Score 183.5; DB 19; Length 131;  
 Best Local Similarity 35.5%; Pred. No. 5.9e-12;  
 Matches 44; Conservative 15; Mismatches 48; Indels 17; Gaps 5;

OY 11 MALLLAGYGVLTGASSGNLRTFGCAVREFFLAKKPGCR-GLRITTDACWGRCETWEK 69  
 Db 7 lllmllsvgvg-wasgyrlp--crpinalaekacpvcitftscagycpsmkrv 63  
 OY 70 -----PILPPYIEAHNRVCTYNEKQVTVKLPNCAPGVDPFTYVPAIRCDGACSTA 123  
 Db 64 vmpalpelpip-----vctylhelrfasvrlpgcpvydpmvstfpvalschgcgpcqjk 116  
 OY 124 TTEG 127  
 Db 117 ttdc 120

RESULT 14  
 AAM47025  
 ID AAM47025 standard; protein: 134 AA.  
 AC AAM47025;  
 XX

```
XX 11-MAY-1998 (first entry)
DT
XX eCG hormone beta-subunit variant (1-134 amino acid residues).
DE
XX Equine; chorionic gonadotropin; hormone; eCG; beta-subunit; treatment;
KW follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;
KM ovarian disease; variant.
XX
OS Family Equidae.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..134
FT /note= "mature protein"
FT
XX
XX JP10036399-A.
XX
XX 10-FEB-1998.
XX
XX 24-JUL-1996; 96JP-0212197.
XX
XX 24-JUL-1996; 96JP-0212197.
XX
XX (ELED ) DENKI KAGAKU KOGYO KK.
XX
XX WPI: 1998-174916/16.
XX
XX Recombinant truncated equine chorionic gonadotropin hormone - has
PT enhanced follicle-stimulating hormone activity and reduced
PT luteinising hormone activity; useful as ovulation inducer
XX
XX Claim 6; Page -: 16pp; Japanese.
XX
XX This is a variant of the beta-subunit of an equine chorionic gonadotropin
CC (eCG) hormone. The variants are created by removing 39 or lesser amino
CC acid residues from the C-terminal peptide region of the beta-subunit. The
CC recombinant eCG hormone is composed of alpha-subunit and the variant
CC beta-subunits of eCG hormone and has a substantially enhanced follicle-
CC stimulating hormone (FSH) activity and reduced luteinising hormone (LH)
CC activity. The hormone is an ovulation inducer and can be used as an
CC agent for the treatment of ovarian diseases.
CC Note: This sequence does not appear in the specification. It has been
CC created by modifying the eCG beta-subunit sequence provided in Page 11.
XX
XX Sequence 134 AA;
SQ
Query Match 25.4%; Score 183.5; DB 19; Length 134;
Best Local Similarity 35.5%; Pred. No. 6e-12; Mismatches 48; Indels 17; Gaps 5;
Matches 44; Conservative 15;
OY 11 MALLLLAGYCVLGASSGNLRTFVGCAVREFTLAKKPGCR-GLRITTDACWRCETWEK 69
DB 7 11wmllsvgy-wasrplrp1--crplnatlaeakeapciftftsicagypsrmvr 63
OY 70 -----PILPEPYIFAHNRVCTYNETKQYTKLPNCAGVDPFFYYPAIRKDCGACSTA 123
DB 64 vmpaalp1p1p-----vclyrelrfsatrlpccppvdpmsvfvalschgcpgq1k 116
OY 124 TTEC 127
DB 117 ttdc 120
```

```
RESULT 15
AAW47026
ID AAW47026 standard; protein; 137 AA.
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XX AAW47026;
XX
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DT 11-MAY-1998 (first entry)
XX
XX eCG hormone beta-subunit variant (1-137 amino acid residues).
DE
XX Equine; chorionic gonadotropin; hormone; eCG; beta-subunit; treatment;
KW follicle-stimulating hormone; FSH; luteinising hormone; LH; ovulation;
KM ovarian disease; variant.
XX
OS Family Equidae.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..137
FT /note= "mature protein"
FT
XX
XX JP10036399-A.
XX
XX 10-FEB-1998.
XX
XX 24-JUL-1996; 96JP-0212197.
XX
XX 24-JUL-1996; 96JP-0212197.
XX
XX (ELED ) DENKI KAGAKU KOGYO KK.
XX
XX WPI: 1998-174916/16.
XX
XX Recombinant truncated equine chorionic gonadotropin hormone - has
PT enhanced follicle-stimulating hormone activity and reduced
PT luteinising hormone activity; useful as ovulation inducer
XX
XX Claim 8; Page -: 16pp; Japanese.
XX
XX This is a variant of the beta-subunit of an equine chorionic gonadotropin
CC (eCG) hormone. The variants are created by removing 39 or lesser amino
CC acid residues from the C-terminal peptide region of the beta-subunit. The
CC recombinant eCG hormone is composed of alpha-subunit and the variant
CC beta-subunits of eCG hormone and has a substantially enhanced follicle-
CC stimulating hormone (FSH) activity and reduced luteinising hormone (LH)
CC activity. The hormone is an ovulation inducer and can be used as an
CC agent for the treatment of ovarian diseases.
CC Note: This sequence does not appear in the specification. It has been
CC created by modifying the eCG beta-subunit sequence provided in Page 11.
XX
XX Sequence 137 AA;
SQ
Query Match 25.4%; Score 183.5; DB 19; Length 137;
Best Local Similarity 35.5%; Pred. No. 6.2e-12; Mismatches 48; Indels 17; Gaps 5;
Matches 44; Conservative 15;
OY 11 MALLLLAGYCVLGASSGNLRTFVGCAVREFTLAKKPGCR-GLRITTDACWRCETWEK 69
DB 7 11wmllsvgy-wasrplrp1--crplnatlaeakeapciftftsicagypsrmvr 63
OY 70 -----PILPEPYIFAHNRVCTYNETKQYTKLPNCAGVDPFFYYPAIRKDCGACSTA 123
DB 64 vmpaalp1p1p-----vclyrelrfsatrlpccppvdpmsvfvalschgcpgq1k 116
OY 124 TTEC 127
DB 117 ttdc 120
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Search completed: July 9, 2002, 13:34:00
Job time: 215 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OK protein - protein search, using sw model

Run on: July 9, 2002, 13:29:15 ; Search time 12.92 Seconds  
(without alignments)  
245.768 Million cell updates/sec

Title: US-09-723-970-1

Perfect score: 722

Sequence: 1 MKLAFLEFLPMALLLAGYG.....VAIRCDGACSTATCECT 130

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	24.7	149	1	US-08-425-673-5 Sequence 5, Appl
2	170	23.5	104	4	US-08-918-288-74 Sequence 74, Appl
3	170	23.5	104	4	US-09-282-357-74 Sequence 74, Appl
4	170	23.5	108	4	US-08-918-288-73 Sequence 73, Appl
5	170	23.5	108	4	US-09-282-357-73 Sequence 73, Appl
6	170	23.5	111	4	US-08-918-288-72 Sequence 72, Appl
7	170	23.5	111	4	US-09-282-357-72 Sequence 72, Appl
8	164	22.7	222	4	US-08-918-288-30 Sequence 30, Appl
9	164	22.7	222	4	US-09-282-357-30 Sequence 30, Appl
10	164	22.7	223	4	US-08-918-288-27 Sequence 27, Appl
11	164	22.7	223	4	US-09-282-357-27 Sequence 27, Appl
12	164	22.7	229	4	US-08-918-288-12 Sequence 12, Appl
13	164	22.7	229	4	US-09-282-357-12 Sequence 12, Appl
14	162	22.4	234	4	US-08-918-288-9 Sequence 9, Appl
15	162	22.4	234	4	US-09-282-357-9 Sequence 9, Appl
16	161	22.3	111	1	US-08-425-673-3 Sequence 3, Appl
17	161	22.3	111	1	US-08-425-673-4 Sequence 4, Appl
18	157	21.7	181	4	US-08-918-288-36 Sequence 36, Appl
19	157	21.7	181	4	US-09-282-357-36 Sequence 36, Appl
20	156	21.6	131	6	US-09-282-357-36 Patent No. 517193-3
21	155	21.5	114	4	US-08-918-288-71 Sequence 71, Appl
22	155	21.5	114	4	US-09-282-357-71 Sequence 71, Appl
23	155	21.5	234	4	US-08-918-288-6 Sequence 6, Appl
24	155	21.5	234	4	US-08-918-288-21 Sequence 21, Appl
25	155	21.5	234	4	US-08-918-288-24 Sequence 24, Appl
26	155	21.5	234	4	US-09-282-357-6 Sequence 6, Appl
27	155	21.5	234	4	US-09-282-357-21 Sequence 21, Appl

28	155	21.5	234	4	US-09-282-357-24 Sequence 24, Appl
29	155	21.5	237	4	US-08-918-288-18 Sequence 18, Appl
30	155	21.5	237	4	US-09-282-357-18 Sequence 18, Appl
31	155	21.5	265	4	US-08-918-288-3 Sequence 3, Appl
32	155	21.5	265	4	US-08-918-288-39 Sequence 39, Appl
33	155	21.5	265	4	US-09-282-357-3 Sequence 3, Appl
34	155	21.5	265	4	US-08-918-288-39 Sequence 39, Appl
35	152	21.1	165	2	US-08-709-925-2 Sequence 2, Appl
36	152	21.1	165	2	US-08-709-925-2 Sequence 2, Appl
37	152	21.1	165	4	US-08-918-288-15 Sequence 15, Appl
38	151	20.9	237	4	US-09-282-357-15 Sequence 15, Appl
39	151	20.9	307	4	US-08-804-166-4 Sequence 4, Appl
40	145.5	20.2	307	4	US-08-910-991-4 Sequence 1, Appl
41	145.5	20.2	345	1	US-08-298-1898-1 Sequence 1, Appl
42	144	19.9	144	4	US-08-918-288-69 Sequence 69, Appl
43	143	19.8	114	4	US-09-282-357-69 Sequence 69, Appl
44	143	19.8	144	1	US-08-475-213-10 Sequence 10, Appl
45	143	19.8	145	1	

## ALIGNMENTS

RESULT 1  
US-08-425-673-5  
; Sequence 5, Application US/08425673  
; Patent No. 5508261  
; GENERAL INFORMATION:  
; APPLICANT: Moyle, William R.  
; ATTORNEY/AGENT INFORMATION:  
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
; TITLE OF INVENTION: Methods For Preparing and Using Same  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Richard R. Muccino  
; STREET: P.O. Box 1267  
; CITY: Princeton  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08551  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,673  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/717,151  
; FILING DATE: 18-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muccino, Richard R.  
; REGISTRATION NUMBER: 32,538  
; TELEPHONE: (609) 466-3407  
; TELEFAX: (609) 466-2760  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 149 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-425-673-5

Query Match 24.7%; Score 178; DB 1; Length 149;  
Best Local Similarity 35.8%; Pred. No. 2.1e-12;

	Matches	39;	Conservative	13;	Mismatches	41;	Indels	16;	Gaps	4;
Oy	26	SSGNRTFVGCAVREFTFLAKKPGCR	-GLRITTDQWCGRCETWEK	-----	PILEPYTE	78				
Db	1	SRGPIRLP	-CRPIATLAEEKKAPICITFTTSLCAGCPSMNVMPALPAIRIQP	----		55				
Oy	79	AHHRCTINERKQYVTKLPNCAGVDPEFTTYVVALRCDGAGCATTEC				127				
Db	56	----	-VCTRLRELFASIRLPGCPGVDPAWSEFVALSCHGPGQIITDD			100				

RESULT 2

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US-08-918-288-74
Sequence 744, Application us/08918288
Patent No. 6238890
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 55000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Muraishige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050,25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-74

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Query Match	23.5%;	Score 170;	DB 4;	Length 104;
Best Local Similarity	37.5%;	Pred. No. 1.1e-11;		
Matches 36;	Conservative 14;	Mismatches 38;	Indels 8;	Gaps 4;

[illegible]

RESULT 3  
US-09-282-357-74  
; Sequence 74, Application US/09282357

### RESULT 3

Patent NO. 0242560  
GENERAL INFORMATION:  
APPLICANT: BOIME, Irving  
APPLICANT: MOYLE, William R.  
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE  
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/282,357  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/918,288  
FILING DATE: 25 AUG-1997  
APPLICATION NUMBER: 08/853,524  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: 08/199,382  
FILING DATE: 18-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Murshige, Kate H  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 29500-20050.25  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500  
TELEFAX: 202-887-0763  
TELEX:  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Query Match	23.5%;	Score 170;	DB 4;	Length 104;
Best Local Similarity	37.5%;	Pred. No. 1.1e-11;		
Matches 36;	Conservative 14;	Mismatches 38;	Indels 8;	Gaps 4;

[illegible]

## RESULT 4

US-08-918-288-/3  
Sequence 783, Application US/08918288  
Patent No. 6238890  
GENERAL INFORMATION:  
APPLICANT: BOIME, Irving  
APPLICANT: MOYLE, William R.  
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE  
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET

```
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 73:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 108 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-918-288-73

Query Match 23.5%; Score 170; DB 4; Length 108;
Best Local Similarity 37.5%; Pred. No. 1.1e-11;
Matches 36; Conservative 14; Mismatches 38; Indels 8; Gaps 4;

QY 36 CAVREFFLAKKPCRCGLRITTDACW--GRCEWEKPILEP--PYIAHHRVCTYNETKQ 91
| : | : | | | | | : | : | : | : | : | : | : |
Db 3 CELNITITAVEKEGC-GFCITINTWCAGCYTRDLVYKDPARKIQ--KTCTFKELVY 58

QY 92 VTVKLPNCAGVDPFYYTPVAIRCDGACGACSTATTEC 127
| : | | | | | | | | | | | | | : | : |
Db 59 ETVRVPGCAHHAADSLYTPVATQCHGCKGSDSDTDC 94

RESULT 5
US-09-282-357-73
? Sequence 73, Application US/09282357
? Patent No. 6242580
? GENERAL INFORMATION:
? APPLICANT: BOYLE, Irving
? APPLICANT: MOYLE, William R.
? TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
? TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
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? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/282,357
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/918,288
? FILING DATE: 25 AUG-1997
? APPLICATION NUMBER: 08/853,524
? FILING DATE: 09-MAY-1997
? APPLICATION NUMBER: 08/199,382
? FILING DATE: 18-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Murashige, Kate H
? REGISTRATION NUMBER: 29,959
? REFERENCE/DOCKET NUMBER: 29500-20050.25
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-887-1500
? TELEFAX: 202-887-0763
? TELEX:
? INFORMATION FOR SEQ ID NO: 73:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 108 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-09-282-357-73

Query Match 23.5%; Score 170; DB 4; Length 108;
Best Local Similarity 37.5%; Pred. No. 1.1e-11;
Matches 36; Conservative 14; Mismatches 38; Indels 8; Gaps 4;

QY 36 CAVREFFLAKKPCRCGLRITTDACW--GRCEWEKPILEP--PYIAHHRVCTYNETKQ 91
| : | : | | | | | : | : | : | : | : | : | : |
Db 3 CELNITITAVEKEGC-GFCITINTWCAGCYTRDLVYKDPARKIQ--KTCTFKELVY 58

QY 92 VTVKLPNCAGVDPFYYTPVAIRCDGACGACSTATTEC 127
| : | | | | | | | | | | | | | : | : |
Db 59 ETVRVPGCAHHAADSLYTPVATQCHGCKGSDSDTDC 94

RESULT 6
US-08-918-288-72
? Sequence 72, Application US/08918288
? Patent No. 6238890
? GENERAL INFORMATION:
? APPLICANT: BOYLE, Irving
? APPLICANT: MOYLE, William R.
? TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
? TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
? NUMBER OF SEQUENCES: 83
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW, suite 5500
? City: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/918,288
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/282,357
? FILING DATE:
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US-08-918-288-30

Query Match 22.7%: Score 164; DB 4; Length 222;

Best Local Similarity 36.8%; Pred. No. 1.2e-10; Mismatches 40; Indels 6; Gaps 3;

36 CAVREFTFLAKKPCGR-GLRITTDACWRCETWEKPILEP--PYIEAHHRVCTYNETKOV 92  
21 CELNITITIAIEKECRRCISINTWACAGCYTRDLVYKDPARPKIQ---KCTFKELVYE 77

93 TVKLPCAPGVDPPYTPVPAIRCDCGACSTATTEC 127

78 TVRVGCAHHADSLTYTPVATQCHGKCDSDSTDC 112

US-09-282-357-30

Sequence 30, Application US/09282357  
Patent No. 6242580

GENERAL INFORMATION:

APPLICANT: BOIME, Irving

TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE  
GLYCOPROTEIN HORMONE QUARTER

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/282,357

FILING DATE:  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/918,288

FILING DATE: 25 AUG-1997

APPLICATION NUMBER: 08/853,524

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: 08/199,382

FILING DATE: 18-FEB-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29500-20050.25

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500

TELEFAX: 202-887-0763

TELEX:  
INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:  
LENGTH: 222 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal

US-09-282-357-30

Query Match 22.7%: Score 164; DB 4; Length 222;

Best Local Similarity 36.8%; Pred. No. 1.2e-10; Mismatches 40; Indels 6; Gaps 3;

Matches 35; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

36 CAVREFTFLAKKPCGR-GLRITTDACWRCETWEKPILEP--PYIEAHHRVCTYNETKOV 92

21 CELNITITIAIEKECRRCISINTWACAGCYTRDLVYKDPARPKIQ---KCTFKELVYE 77

93 TVKLPCAPGVDPPYTPVPAIRCDCGACSTATTEC 127

78 TVRVGCAHHADSLTYTPVATQCHGKCDSDSTDC 112

US-08-918-288-27

Sequence 27, Application US/08918288  
Patent No. 6238890

GENERAL INFORMATION:

APPLICANT: BOIME, Irving

TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE  
GLYCOPROTEIN HORMONE QUARTER

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW, suite 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/918,288

FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/282,357

FILING DATE:

APPLICATION NUMBER: 08/853,524

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: 08/199,382

FILING DATE: 18-FEB-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29500-20050.25

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-887-1500

TELEFAX: 202-887-0763

TELEX:  
INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal

US-08-918-288-27

Query Match 22.7%: Score 164; DB 4; Length 223;

Best Local Similarity 36.8%; Pred. No. 1.2e-10; Mismatches 40; Indels 6; Gaps 3;

Matches 35; Conservative 14; Mismatches 40; Indels 6; Gaps 3;

36 CAVREFTFLAKKPCGR-GLRITTDACWRCETWEKPILEP--PYIEAHHRVCTYNETKOV 92

21 CELNITITIAIEKECRRCISINTWACAGCYTRDLVYKDPARPKIQ---KCTFKELVYE 77

93 TVKLPCAPGVDPPYTPVPAIRCDCGACSTATTEC 127

78 TVRVGCAHHADSLTYTPVATQCHGKCDSDSTDC 112

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1 RESULT 11
2 US-09-282-357-27
3 ; Sequence 27, Application US/09282357
4 ; Patent No. 6242580
5 ; GENERAL INFORMATION:
6 ; APPLICANT: BOIME, Irving
7 ; APPLICANT: MOYLE, William R.
8 ; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
9 ; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
10 ; NUMBER OF SEQUENCES: 83
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: MORRISON & FOERSTER
13 ; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
14 ; City: Washington
15 ; STATE: DC
16 ; COUNTRY: USA
17 ; ZIP: 20006-1888
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Diskette
20 ; COMPUTER: IBM Compatible
21 ; OPERATING SYSTEM: DOS
22 ; SOFTWARE: FASTSEQ for Windows Version 2.0
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/09/282.357
25 ; FILING DATE:
26 ; CLASSIFICATION: 536
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: 08/918, 288
29 ; FILING DATE: 25 AUG-1997
30 ; APPLICATION NUMBER: 08/853,524
31 ; FILING DATE: 09-MAY-1997
32 ; APPLICATION NUMBER: 08/199,382
33 ; FILING DATE: 18-FEB-1994
34 ; ATTORNEY/AGENT INFORMATION:
35 ; NAME: Murashige, Kate H
36 ; REGISTRATION NUMBER: 29,959
37 ; REFERENCE/DOCKET NUMBER: 22500-20050.25
38 ; TELECOMMUNICATION INFORMATION:
39 ; TELEPHONE: 202-887-1500
40 ; TELEFAX: 202-887-0763
41 ; TELEX:
42 ; INFORMATION FOR SEQ ID NO: 27:
43 ; SEQUENCE CHARACTERISTICS:
44 ; LENGTH: 223 amino acids
45 ; TYPE: amino acid
46 ; STRANDEDNESS: single
47 ; TOPOLOGY: linear
48 ; MOLECULE TYPE: protein
49 ; FRAGMENT TYPE: internal
50 ;
51 US-09-282-357-27
52
53 Query Match 22.7%; Score 164; DB 4; Length 223;
54 Best Local Similarity 36.8%; Pred No. 1.2e-10;
55 Matches 35; Conservative 14; Mismatches 40; Indels 6; Gaps 3;
56
57 QY 36 CAVREFTFLAKPGGR-GIRITTDACWGRCEETWERPILEP--PYIEAHHRVCTYNETKOV 92
58 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
59 Db 21 CELTMTITIAIEKEBERFCISINTTMCAGCYTRDLVYKDPARKIQ---KIQTFKELIYVE 77
60 | : | | | | | | | | | | | | | | | | | : | : | : | : |
61 QY 93 TVKLPNCARGVDPEYTYPAVAIRCDCGACSTATTEC 127
62 | : | | | | | | | | | | | | | | | | | : | : | : | : |
63 Db 78 TVRPDGAHHAADSLYTPVATQCHGKCDSDSTDC 112
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65 RESULT 12
66 US-08-918-288-12
67 ; Sequence 12, Application US/08918288
68 ; Patent No. 6238890
69 ; GENERAL INFORMATION:
70 ; APPLICANT: BOIME, Irving
71 ; APPLICANT: MOYLE, William R.
72 ; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE

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1 TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
2 NUMBER OF SEQUENCES: 83
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: MORRISON & FOERSTER
5 STREET: 2000 Pennsylvania Avenue, NW, suite 5500
6 CITY: Washington
7 STATE: DC
8 COUNTRY: USA
9 ZIP: 20006-1688
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette
12 COMPUTER: IBM Compatible
13 OPERATING SYSTEM: DOS
14 SOFTWARE: FastSeq for Windows Version 2.0
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/918,288
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 09/282,357
21 FILING DATE:
22 APPLICATION NUMBER: 08/853,524
23 FILING DATE: 09-MAY-1997
24 APPLICATION NUMBER: 08/199,382
25 FILING DATE: 18-FEB-1994
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Murashige, Kate H
28 REGISTRATION NUMBER: 29,959
29 REFERENCE/DOCKET NUMBER: 29500-20050.25
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 202-887-1500
32 TELEFAX: 202-887-0763
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Tue Jul 9 13:45:45 2002

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Page 8

FILING DATE: 25 AUG-1997  
 APPLICATION NUMBER: 08/853,524  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: 08/199,382  
 FILING DATE: 18-FEB-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Murashige, Kate H  
 REGISTRATION NUMBER: 29,959  
 REFERENCE/DOCKET NUMBER: 29500-20050.25  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-887-1500  
 TELEFAX: 202-887-0763  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 234 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 OS-09-282-357-9

Query Match	22.4%	Score 163;	DB 4;	Length 234;
Best Local Similarity	33.6%	Pred. No. 2.2e-10;		
Matches 41; Conservative	21;	Mismatches 50;	Indels 10;	Gaps 5;

[illegible]

Search completed: July 9, 2002, 13:33:23  
Job time: 248 sec



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Db      59    PSMKRVLEVLPEPMQ---RVCITYELHFRASVRLGCGPBGVDPMWSPFVALSCHGCPCL 115
OY      123    ATTEC 127
          ::| |
          116    SSTDC 120

RESULT   2
UTCA8
gonadotropin beta chain precursor - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 31-Aug-1979 #sequence_revision 16-Feb-1996 #text_change 23-Mar-2001
C:Accession: S29677; S29678; JT0462; A01504
R:Chang, Y.S.; Huang, F.L.; Lo, T.B.
submitted to the EMBL Data Library, May 1991
A:Reference number: S29677
A:Accession: S29677
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <CH>
A:Cross-references: EMBL:X59888; NID:g62619; PIDN:CAA42542.1; PID:g62620
A:Accession: S29678
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <CH>
A:Cross-references: EMBL:X59889; NID:g62621; PIDN:CAA42543.1; PID:g62622
R:Chang, Y.S.; Huang, C.J.; Huang, F.L.; Lo, T.B.
Int. J. Pept. Protein Res. 32, 556-564, 1988
A>Title: Primary structures of carp gonadotropin subunits deduced from cDNA nucleotide s
A:Reference number: JK0024; MUID:89233593
A:Accession: JT0462
A:Molecule type: mRNA
A:Residues: 1-144 <CH2>
R:Jolles, J.; Burzawa-Gerard, E.; Fontaine, Y.A.; Jolles, P.
Biochimie 59, 893-898, 1977
A>Title: The evolution of gonadotropins: some molecular data concerning a non-mammalian
A:Reference number: A80673; MUID:76124308
A:Accession: A01504
A:Molecule type: protein
A:Residues: 28-36,'X',38-53;141-142 <JOL>
C:Genetics:
A:Introns: 6/2; 65/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; pituitary
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-117/Product: gonadotropin beta chain #status predicted <MAT>
F:33-58,47-81,50-112,62-134,96-124,114-117/Disulfide bonds: #status predicted
F:37/Binding site: carbonydrate (Asn) (covalent) #status predicted

Query Match       28.9%; Score 209; DB 1; Length 144;
Best Local Similarity 42.5%; Pred. No. 2e-13;
Matches 37; Conservative 17; Mismatches 31; Indels 2; Gaps 2;

OY      42    TELAKKPGC-RGLRTITDRCGRCEMEKEPILEPPYIEAHHRVCYNENKTQVTKLPNCA 100
          | :||| : :| :| ||::|| : :||| : :||| : :|||::| :|:|:|
DB      39    TVAVEEGECPRKCLIVQTTCISGHCLT-KEPYVKSPFSFYQHVCIRDYRETVRLPDCC 97
          ||||| ||||| ||| : :||| : :||| : :||| : :||| : :||| : :|||

OY      101   PGVDPPYYPAVAICDDCGACSTATTTC 127
          ||||| ||||| ||| : :||| : :||| : :||| : :||| : :||| : :|||
DB      98    PGVDPHITYPVALSCDCSLCTMDTSDC 124

RESULT   3
B60626
gonadotropin beta chain precursor - silver carp
C:Species: Hypophthalmichthys molitrix (silver carp)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B60626
R:Chang, Y.S.; Huang, C.J.; Huang, F.L.; Liu, C.S.; Lo, T.B.
Gen. Comp. Endocrinol. 78, 23-33, 1990
A>Title: Purification, characterization, and molecular cloning of gonadotropin subunits
A:Reference number: A60626; MUID:90236229

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A:Accession: B60626
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141 <CHNA>
A:Note: parts of this sequence, including the amino and carboxyl ends of the mature p
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-139/Product: gonadotropin beta chain #status experimental <Mat>
F:30-55,44-78,47-109,59-131,93-121,11-114/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          28.7%  Score 207;  DB 1;  Length 141;
Best Local Similarity 42.5%  Pred. No. 3,1e-13;
Matches 37;  Conservative 16;  Mismatches 32;  Indels 2;  Gaps 2;

OY      42  TFLAKKPGC-RGLRITTDACMGRCETWEKPILEPPYIEAHNRVCTYNETKQVTLKPNCA 100
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      36  TVAVEKECCPRKCLVHQTITCSGHCLT-KEPYKSPSFVYGVHCTYRDVRYETVRLDPCP  94
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

OY      101 PGVDPEFTYTPVAIRCDGACGACSTATTEC 127
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      95  PGVDPHITYPVALSCDSCSLCTMDTSDC 121
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT      4
S16763
gonadotropin beta chain - grass carp
C:Species: Ctenopharyngodon idella (grass carp)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S16763
R:Chang, Y.S.; Huang, F.L.; Lo, T.B.
submitted to the EMBL Data Library, July 1991
A:Description: The cDNA cloning and primary structures of grass carp gonadotropin sub
A:Reference number: S16762
A:Accession: S16763
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <CHNA>
A:Cross-references: EMBL:X61051; NID:962708; PIDN:CA043385.1; PID:962709
C:Superfamily: pituitary glycoprotein hormone beta chain
F:35-60,49-83,52-114,64-136,98-126,116-119/Disulfide bonds: #status predicted

Query Match          28.7%  Score 207;  DB 1;  Length 146;
Best Local Similarity 42.5%  Pred. No. 3.2e-13;
Matches 37;  Conservative 16;  Mismatches 32;  Indels 2;  Gaps 2;

OY      42  TFLAKKPGC-RGLRITTDACMGRCETWEKPILEPPYIEAHNRVCTYNETKQVTLKPNCA 100
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      41  TVAVEKECCPRKCLVHQTITCSGHCLT-KEPYKSPSFVYGVHCTYRDVRYETVRLDPCP  99
      1  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

OY      101 PGVDPEFTYTPVAIRCDGACGACSTATTEC 127
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Db      100 PGVDPHITYPVALSCDSCSLCTMDTSDC 126
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RESULT      5
UTSHB
lutropin beta chain precursor - sheep
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C:Accession: I46949; S092332; A92110; A90053; B61096; A01500
C:Brown, P.; McNeill, J.R.; Wallace, R.M.; McNeill, A.S.; Clark, A.J.
Mol. Cell. Endocrinol. 93, 157-165, 1993
A:Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gon
A:Reference number: I46949; MUID:93351742
A:Accession: I46949
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-141 <BRO>

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A:Cross-references: GB:S64695; NID:9408240; PIDN:AA827819.1; PID:9408241  
R.d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.  
Nucleic Acids Res. 18, 2175, 1990  
A>Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subunit  
A:Reference number: 509232; MUID:90245669  
A:Accession: 509232  
A:Molecule type: mRNA  
A:Residues: 1-58, 'L', 60-62, 'O', 64-141 <ANG>  
A:Cross-references: EMBL:X52488; NID:941319; PIDN:CA436729.1; PID:941320  
R.Liu, W.K.; Nahn, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.  
J. Biol. Chem. 247, 4365-4381, 1972  
A>Title: The primary structure of ovine lutelizing hormone. II. The amino acid sequence  
A:Reference number: A92110; MUID:7221145  
A:Accession: A92110  
A:Molecule type: protein  
A:Residues: 21-121, 'PG', 124-125, 'E', 127-139 <LIU>  
R.Saitam, M.R.; Samy, T.S.A.; Papkoft, H.; Li, C.H.  
Arch. Biochem. Biophys. 153, 572-586, 1972  
A>Title: The primary structure of ovine interstitial cell-stimulating hormone. II. The b  
A:Reference number: A90053; MUID:73190035  
A:Accession: A90053  
A:Molecule type: protein  
A:Residues: 21-29, 'E', 31-71, 'P', 72-80, 'Q', 82-121, 'PG', 124-125, 'E', 127-139 <SAI>  
R.Nomura, K.; Tsunashima, S.; Ohnura, K.; Sakiyama, F.; Shizume, K.  
Endocrinology 123, 700-712, 1988  
A>Title: Renotropic activity in ovine lutelizing hormone isoform(s).  
A:Reference number: A61098; MUID:88283534  
A:Accession: A61098  
A:Molecule type: protein  
A:Residues: 21-39, 'N', 41-49, 64-78, 'V', 80-82, 84-106, 115-121, 'PG', 124-138 <NOM>  
A>Note: This form was designated form beta-3; forms beta-1 and beta-2 each lack several  
C:Genetics:  
A:introns: 5/3; 61/3  
C:Superfamily: pituitary glycoprotein hormone beta chain  
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-14/Product: lutropin beta chain #status experimental <MAT>  
F:21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acetyla  
F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/disulfide bonds: #status predicted  
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match          27.9%; Score 201.5; DB 2; Length 140;
Best Local Similarity 38.9%; Pred. No. 1.1e-12;
Matches 42; Conservative 16; Mismatches 47; Indels 3; Gaps 3;

OY      21 CVLGASGNLRFVFCACAREFTFLAKKPGC-RGLRITTDACMGRCETWEKPPIEPTIEA 79
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      16 CHLVASAG-SLLLPCEPINEFISVENKDCPKCLVFQSISSGHCHT-KDPSYKSPLSTV 73
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      80 HHRCTYETEKOVTVKLPCNAPGVDPFYTYVAIRCDGACSTRATEC 127
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      74 YORVTGYDRVRETVRLPDRCRPVDPHVTFPVALSCDNLCTMDTSDC 121
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      7
C36179      gonadotropin II beta chain precursor - chum salmon
C:Species: Oncorhynchus keta (chum salmon)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: C36179; S09344
R:Sekine, S.; Saico, A.; Itoh, H.; Kawauchi, H.; Itoh, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 8645-8649, 1989
A:title: Molecular cloning and sequence analysis of chum salmon gonadotropin cDNAs.
A:Reference number: A36179; MUID:90046849
A:Accession: C36179
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <SEQ>
A:Cross-references: GB:M27154; NID:g213429; PIDN:AAA4940.1; PID:g213430
R:Itooh, H.; Suzuki, K.; Kawauchi, H.
Gen. Comp. Endocrinol. 71, 438-451, 1988
A:title: The complete amino acid sequences of beta-subunits of two distinct chum salm
A:Reference number: S07216; MUID:85053031
A:Accession: S09344
A:Molecule type: protein
A:Residues: 24-72, 'I', 74-142 <ITO>
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein, heterodimer, hormone, pituitary
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-142/Product: gonadotropin II beta chain #status experimental <MAT>
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          27.8%; Score 201; DB 1; Length 142;
Best Local Similarity 34.7%; Pred. No. 1.2e-12;
Matches 42; Conservative 19; Mismatches 44; Indels 16; Gaps 3;

OY      22 VVLGASSGLRFRFGCAVE-----FFLAKKRGCC-RGLRITTDACMGRET 66
       :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db      1 MGLHVGILSLIFLCILLEPEVGSIMQCPINOTVSLEKGCPTCIYIPITSGHCYT 60
       :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

OY      67 WEKPIPEIAEHHRVCTNETKOVTVKLPCNAPGVDPFYTYVAIRCDGACSTATTE 126
       ::||:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db      61 KEPIFKRPFESTVOHVCTYRDVRETRIRLDPCPPWDPHVTYPVALSCDCLCMOTSD 119
       :|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

OY      QY      127 C 127
       |
Db      Db      120 C 120

RESULT      8
150554      gonadotropin II beta subunit - mummichog
C:Species: Fundulus heteroclitus (mummichog)
C:date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: 150554
R:Llin, T.W.; Rapnow, B.A.; Price, D.A.; Greenberg, R.M.; Wallace, R.A.
Mol. Cell. Endocrinol. 85, 127-139, 1992
A:title: Fundulus heteroclitus gonadotroplns. 3. Cloning and sequencing of gonadotrop
A:Reference number: 150553; MUID:92405806
A:Accession: 150554
A:Status: preliminary; translated from GR/EMBL/DDB1
A:Molecule type: mRNA
```



RESULT 13  
150143  
gonadotropin II beta chain - arctic cisco  
C:Species: Coregonus autumnalis (arctic cisco)  
C:Date: 21-Feb-1997 #sequence\_rev:150143  
C:Accession: 150143  
R:ItolimoVA, I.N.; Belikov, S.I.  
Mol. Biol. (Mosk.) 28, 1052-1056, 1994  
A:Title: [Cloning and sequencing the cDNA for the beta-subunit of Baikal omul gonadotropin]  
A:Reference number: 150143; MUID:95082790  
A:Accession: 150143  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-142 <TRO>  
A:Cross-references: GB:U23431; NID:g387920; PIDN:AAA66207.1; PID:g387921  
C:Genetics:  
A:Gene: GTH-II  
A:Superfamily: pituitary glycoprotein hormone beta chain

[illegible]

```

RESULT      14
A:25800
gonadotropin beta chain precursor - chinook salmon
C:Species: Oncorhynchus tshawytscha (chinook salmon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A25800
R:Rtinh, K.Y.; Wang, N.C.; Hew, C.L.; Crim, L.W.
Eur. J. Biochem. 159, 619-624, 1986
A:Title: Molecular cloning and sequencing of salmon gonadotropin beta subunit.
A:Reference number: A25800; MUID:87004682
A:Accession: A25800
A:Molecule type: mRNA
A:Residues: 1-142 <RR1>
A:Cross-references: GB:X04404; NID:664202; PIDN:CAA27992.1. PID:664203
C:Superfamily: pituitary glycoprotein hormone beta chain
F:29-56,43-77,46-106,56-130,92-120,110-113/Disulfide bonds: #status predicted

```

```

Query Match      25.5%  Score 184:  DB 1:  Length 142;
Best Local Similarity 32.2%  Pred. No. 5.6e-11;
Matches 39;  Conservative 19;  Mismatches 47;  Indels 16;  Gaps 3.

Qy      22  VLGASGSLRFFVGCAYRE-----FFFLAKKPGC-RGLRITTDACWGRCET 66
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      1  MLGHLVGLILFLFCLILEPGLSGLMOPCQPIRQNVSLLEKECPCLVIATICSHCYT 60

Qy      67  WEKPILEPPIYEAHHRYCTVNETKQVTLKLPNCAGVDPFYTYRVAIRDCGAGCSTATTE 126
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      61  -KEPVKSPFSTVYQHVCYTRDVRVREMIRLPDCCPWSPPHYTYRVALSDCSLCNMNDS 119

Qy      127  C 127
Db      120  C 120

```

choriogonadotropin beta chain precursor - horse  
N:Alternate names: chorionic gonadotropin beta chain (CG); luteinizing hormone (LH) beta  
;Species: Equus caballus (domestic horse)

```

C:Date: 14-Nov-1983 #sequence.revision:03-May-1996 #text_change:18-Jun-1999
C:Accession: A41917: A29304: A29305: A01503
R:Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.
Mol. Endocrinol. 6, 951-959, 1992
A>Title: A single site encodes the beta-subunits of equine luteinizing hormone and ch
A:Reference number: A41917: MUID:92357035
A:Accession: A41917
A:Molecule type: DNA
A:Residues: 1-169 <SHE>
A:Cross-references: GB:S41704; NID:g252740; PIDN:AMB22775.1; PID:g252741
A:Experimental source: sperm
A>Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBIIP:110185)
R:Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.
J. Biol. Chem. 262, 8603-8609, 1987
A>Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29304; MUID:87250475
A:Accession: A29304
A:Molecule type: protein
A:Residues: 21-169 <SUG>
R:Bousfield, G.R.; Iku, W.K.; Sugino, H.; Ward, D.N.
J. Biol. Chem. 262, 8610-8620, 1987
A>Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29305; MUID:87250476
A:Accession: A29305
A:Molecule type: protein
A:Residues: 21-169 <BOU>
R:Ward, D.N.; Moore Jr., W.T.; Bursleigh, B.D.
J. Protein Chem. 1, 263-280, 1982
A>Title: Structural studies on equine chorionic gonadotropin.
A:Reference number: A01503
A:Accession: A01503
A:Molecule type: protein
A:Residues: 21-40,'C',42-43,'SK',46,'XXXX',51,'T',53-64,'T',66-96,'B',98,'R',100-102,'
R:Matsu, T.; Mizunochi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sugl
Biochemistry 33, 14039-14048, 1994
A>Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot
A:Reference number: A59592; MUID:95034847
A:Contents: annotation; glycosylation
A>Note: horse lutropin and chorionadotropin beta chains have identical protein chain
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-169/Product: chorionadotropin beta chain #status experimental <MAT>
F:20-77,'43'-92,'46'-130,'54'-108,'58'-110,'113'-120/Duplicate bonds: #status predicted
F:33/Binding site: carbohydrate (asn) (covalent) #status experimental

```

	Query Match	25.4%	Score 183.5;	DB 1;	Length 169;
	Best Local Similarity	35.5%	Pred. No. 7.5e-11;		
	Matches	44;	Conservative	15;	Mismatches 48; Indels 17; Gaps
QY	11	MAILLLAGGCVLGASSGNLTFTFGCAVREFTEFLAKKRGCR-GHRTTTDQCWGRCEIWEK	69		
	:	: : :	:	:	:
Db	7	LLEMLLISGVG-VASNGPLRPL--CAPINATLAAEKEACPICITFTTSCAGYCPSMR	63		
QY	70	-----PILEEPTYEAAHHRCCTYMETQAVYVKLPENCAPGDVPTTYTVVAIRCDGACSTA	123		
	:	: : :	:	:	:
Db	64	VMPALPAIPQP-----VCTYRELTFASRIPLGPCPDVMVSFPVALSCHCGPCQIK	116		
QY	124	TTEC 127			
	:	: : :			
Db	117	TTDC 120			

Search completed: July 9, 2002, 13:34:22  
Job time: 212 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 13:34:05 ; Search time 11.87 Seconds  
(without alignments)  
424.056 Million cell updates/sec

Title: US-09-723-970-1  
Perfect score: 722  
Sequence: 1 MKLAFLEFLGPMALLLAGYG.....VAIRDCGACSTATTECETI 130

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213.5	29.6	149	1	GTH2_CLUPA
2	210	29.1	141	1	LSHB_BOVIN
3	209	28.9	140	1	GTH2_CARAU
4	209	28.9	144	1	GTH2_CYPCA
5	207	28.7	141	1	GTH2_HYPMO
6	207	28.7	146	1	GTH2_CTEID
7	204	28.3	138	1	GTH2_CLAGA
8	202.5	28.0	141	1	LSHB_SHEEP
9	201.5	27.9	140	1	GTH2_ANGAN
10	199	27.6	142	1	GTH2_ANGKE
11	199	27.4	136	1	GTH2_FUNHE
12	198	27.3	113	1	GTHB_MURCI
13	197	27.3	115	1	GTH2_THROB
14	196	27.1	107	1	FSHB_RANCA
15	192	26.6	142	1	GTH2_ONCMA
16	189	26.2	112	1	LSHB_RANCA
17	189	26.2	139	1	GTH2_MORSA
18	186.5	25.8	142	1	GTH2_CORAU
19	186.5	25.8	169	1	LSHB_BOVBU
20	184.5	25.6	169	1	LSHB_EOUAS
21	184	25.5	142	1	GTH2_EOUAS
22	184	25.5	146	1	GTH2_TRITC
23	183.5	25.4	169	1	LSHB_HORSE
24	181	25.1	137	1	GTH2_ACALA
25	180.5	25.0	141	1	LSHB_CERST
26	178	24.7	128	1	LSHB_PROSU
27	178	24.7	141	1	LSHB_RAT
28	176	24.4	141	1	LSHB_TRIVU
29	175	24.2	126	1	FSHB_PHOSU
30	175	24.2	141	1	LSHB_MOUSE
31	174	24.1	141	1	LSHB_PIG
32	173	24.0	138	1	LSHB_MACRU
33	172.5	23.9	138	1	LSHB_CANFA

34	171	23.7	147	1	FSHB_ANGAN	Q08127 anguilla an
35	167	23.1	129	1	FSHB_CAVPO	Q91K69 cavia porce
36	165	22.9	118	1	LSHB_BALAC	P33088 balaenopter
37	164	22.7	128	1	LSHB_STRCA	P80664 struthio ca
38	164	22.7	129	1	FSHB_HUMAN	P01225 homo sapien
39	164	22.7	129	1	FSHB_TRIVU	Q06887 trichosurus
40	164	22.7	130	1	FSHB_MOUSE	Q06887 mus musculu
41	163.5	22.6	143	1	FSHB_FELCA	P7805 felis silve
42	163	22.6	130	1	FSHB_RAT	P18427 rattus norv
43	162	22.4	129	1	FSHB_PIG	P01228 sus scrofa
44	162	22.4	141	1	LSHB_HUMAN	P01229 homo sapien
45	161	22.3	118	1	LSHB_PHYCA	P25330 physeter ca

ALIGNMENTS

RESULT 1  
GTH2\_CLUPA  
ID GTH2\_CLUPA STANDARD; PRT; 149 AA.  
AC 09YGH2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Gonadotropin beta-II chain precursor (GTH-II-beta).  
OS Clupea pallasi (Pacific herring).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;  
OC Clupeinae; Clupea.  
OX NCBI\_TaxID=30724;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=pituitary;  
RA Power M.E., Carolisfield J., Wallis G.P., Sherwood N.M.:  
RT "Isolation and characterization of a cDNA for gonadotropin II-beta of Pacific herring, an ancient teleost."  
RL J. Fish Biol. 50:315-323(1997).  
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.  
CC -----  
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CC -----  
CC EMBL: X91984; CAA63038.1; -  
DR HSSP; P01233; 1XU.  
DR InterPro; IPR000359; Cys\_knot.  
DR InterPro; IPR001545; Glyco\_hormone\_beta.  
DR Pfam; PF00007; Cys\_knot; 1.  
DR SMART; SM00068; GHb; 1.  
DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
KW Hormone; Glycoprotein; Signal.  
FT SIGNAL 1 24  
FT CHAIN 1 149  
FT DISULFID 30 78  
FT DISULFID 44 93  
FT DISULFID 47 131  
FT DISULFID 55 109  
FT DISULFID 59 111  
FT DISULFID 114 121  
FT CARBOHYD 34 34  
SO SEQUENCE 149 AA; 16627 MW; 4585DCB34367069 CRC64;  
N-LINKED (GLCNAC...) (POTENTIAL).  
Query Match 29.6%; Score 213.5; DB 1; Length 149;  
Best Local Similarity 38.8%; Pred. No. 3,2e-15;

```

Matches 47; Conservative 18; Mismatches 49; Indels 7; Gaps 4;
QY 10 PMALLLLAGYCYLGG-ASSGNLRTFYVCAAREFFFLAKKPEG-RGLRTTDDACKRGRET 66
Db 5 PECTLLTLLCMCVLAVPACQFENLP--CLVNETVSVKEKCPRLVFRRTTSGHCPT 61
QY 67 WEKPLEPPTLEAHHRVCTYNETKGVTKLPKACAGVPPEFYYPVPAIKDCGACSTATTE 126
Db 62 -KEPYKRSFVSFVNGHVCTYGNFRFETIRLPDCAAGVDPPLVITYYPALSGECSLCMDISD 120
QY 127 C 127
Db 121 C 121

RESULT 2
LSHB_BOVIN STANDARD; PRT; 141 AA.
ID LSHB_BOVIN
AC P04651;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomson A.R., Nilsson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes
RL a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RN J. Biol. Chem. 260:7072-7077(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85182575; PubMed=3838746;
RA Maurer R.A.;
RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
RL heterogeneity in nucleotide sequence.";
RN J. Biol. Chem. 260:4684-4687(1985).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maguin-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
RL bovine and porcine species.";
RN Eur. J. Biochem. 39:235-253(1973).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; M10077; AAA30623.1; -.
CC EMBL; M11506; AAB59267.1; -.
CC PIR; A01499; UTBOB.
CC HSSP; P01233; 1XUL.
CC GlycoSuiteDB; P04651; -.
CC InterPro; IPR000359; Cys_Knot.

```

```

DR InterPro: IPR002440; GF_cys_knot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot_1.
DR PRINTS: PR00438; GFCYSKNOT.
DR SMART: SMO0068; GHF; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR DR PROSITE: PS00689; GLYC_HORMONE__BETA_2; 1.
KW Hormone; signal; glycoprotein..
FT SIGNAL                     1          20
FT CHAIN                      21         141    LUTROPIN BETA CHAIN.
FT DISULFID                   29           77      BY SIMILARITY.
FT FT                          43           92      BY SIMILARITY.
FT DISULFID                    46          130      BY SIMILARITY.
FT DISULFID                    54          108      BY SIMILARITY.
FT FT                          58          110      BY SIMILARITY.
FT DISULFID                    113          120      BY SIMILARITY.
FT CARBOHYD                   33            33        N-LINKED (GLCNAc...), /FTID-CAR_000044.
FT CONFLICT                    1             2     MISSING (IN REF. 2).
FT CONFLICT                    74             74   Q -> E (IN REF. 3).
FT CONFLICT                    112            112   P -> S (IN REF. 2).
FT CONFLICT                    122            123   GP -> PG (IN REF. 3).
FT CONFLICT                    126            126   O -> E (IN REF. 3).
SQ SEQUENCE                  141 AA; 15202 MW; 4AFBICBD4901BC95 CRC64;

Query Match               Best Local Similarity       39.1%; Score 210; DB 1; Length 141;
Matches 48; Conservative 28.4%, Pred. No. 6,ge-15; Mismatches 46; Indels 10; Gaps 5.

QY 6 FLFLGPMALLLLAGVCVLAGSSGNIRTEVGCAVRREFTLAKRGR-GLRITTDACWGRC 64
DB 3 MFQGILLWLLLGVAG--VWASRGRLPL--CGPINATAAEACAPCVCTFFTSICAGYC 58
QY 65 ETWEK--FILRRPYIEAHHRCTYEHTNQVKTLNCAFGVPFRPTTPAINDGCAGST 122
DB 59 PSMRKVLDPVLPMPMD--RVCTYHELFRAVSRLFPGCPGDVMWSFPVALSCHGPCL 115
QY 123 ATTEC 127
DB 116 SSTDC 120

RESULT      3
GTH2_CARAU ID GTH2_CARAU STANDARD; PTR; 140 AA.
AC Q98849;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta) [lutelizing hormone-like gth].
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprindae; Carassius.
OX NCBI_Taxid=7957;
RN R[1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary; PubMed=9073500; MEDLINE=97242868;
RX yoshiura Y., Kobayashi M., Kato Y., Aida K.; "Molecular cloning of the cDNAs encoding the gonadotropin beta subunits (GTH-I beta and -II beta) from the goldfish, Carassius auratus.";
RT Gen. Comp. Endocrinol. 105:379-389(1997).
RN RN R[2]
RP SEQUENCE FROM N.A.
RC Sohn Y.C., Yoshiura Y., Suetsake H., Kobayashi M., Aida K.; "Nucleotide sequence of gonadotropin II beta subunit gene in goldfish.";
RT Fisheries Sci. 65:800-801(1999).
NC -I- FUNCTION INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
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Query Match	Best Local Similarity	28.7%; Score 207; DB 1; Length 141;
Matches	37; Conservative	16; Mismatches 32; Indels 2; Gaps 2.
QY 42	TEFAKPGC-RGLRITTTACMGRCETWEKPLEPPYIEAHNHVCYNETKQYVKLPNCA	100
DB 36	TYAVEKEGPKRLVQTITCSGHCLT-KRPYKSPESITYGIVCYRVDYRETVRLPDCP	94
OY 101	PGVDPPYTPVAIRCDGCGASTATTEC	127
DB 95	PGVDHITTPVALSCDCSICLTMDTSDC	121
RESULT 6		
GT_H2_CREID	STANDARD:	PRT; 146 AA.
ID GT_H2_CREID		
AC P30984;		
DT 01-JUL-1993 (Rel. 26, Created)		
DT 01-JUL-1993 (Rel. 26, Last sequence update)		
DT 16-OCT-2001 (Rel. 40, Last annotation update)		
DE Gonadotropin beta-II chain precursor (GTH-II-beta) (Luteinizing hormone-like GTH) (Fragment).		
OS Ctenopharyngodon idella (Grass carp).		
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC Cypriniformes; Cyprinidae; Ctenopharyngodon.		
CC Cypriniformes; Cyprinidae; Ctenopharyngodon.		
NCBI_TaxID=7959;		
NCBI_TaxID=7959;		
SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.		
RA Chang Y.S., Huang C.J., Huang F.-L., Liu C.S., Lo T.-B.;		
RT "Purification, characterization, and molecular cloning of gonadotropin subunits of silver carp (Hypophthalmichthys molitrix).";		
RL Gen. Comp. Endocrinol. 78:23-33(1990).		
CC -1- SUBUNIT: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.		
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.		
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.		
CC PIR: B60626; B60626.		
DR HSSD: P01233; 1XU.		
DR InterPro: IPR000359; Cys_knot.		
DR InterPro: IPR002400; GF_cysknot.		
DR InterPro: IPR001545; Glyco_hormone_beta.		
DR Pfam: PF00007; Cys_knot; 1.		
DR PRINTS: PR00438; GFCYSKNOT.		
DR SMART: SM00068; GHB; 1.		
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.		
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.		
DR Hormone; Glycoprotein; Signal.		
FT SIGNAL	1 24	
FT CHAIN	25 139	GONADOTROPIN BETA-II CHAIN.
FT PROPEP	140 141	
FT DISULFID	30 78	BY SIMILARITY.
FT DISULFID	44 93	BY SIMILARITY.
FT DISULFID	47 131	BY SIMILARITY.
FT DISULFID	55 109	BY SIMILARITY.
FT DISULFID	59 111	BY SIMILARITY.
FT DISULFID	114 121	BY SIMILARITY.
FT CARBOHD	34 34	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE	141 AA; 15656 MW; A4ZC48FE933EEA46 CRC64;	

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CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
CC DR EMBL: X61051; CAA43385.1; -.
CC DR PIR: S16763; S16763.
CC DR HSPB; P01233; 1XU1.
CC DR InterPro: IPR000359; Cys_knot.
CC DR InterPro: IPR001545; Glyco_hormone_beta.
CC DR Pfam: PF00007; Cys_knot; 1.
CC DR SMART: SM00068; GHb; 1.
CC DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
CC DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
CC KW Hormone; Glycoprotein; Signal.
CC FT NON TER 1 1
CC FT SIGNAL <1 28 BY SIMILARITY.
CC FT CHAIN 29 146 GONADOTROPIN BETA-II CHAIN.
CC FT DISULFID 35 83 BY SIMILARITY.
CC FT DISULFID 49 98 BY SIMILARITY.
CC FT DISULFID 52 136 BY SIMILARITY.
CC FT DISULFID 60 114 BY SIMILARITY.
CC FT DISULFID 64 116 BY SIMILARITY.
CC FT DISULFID 119 126 BY SIMILARITY.
CC FT CARBOHYD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 146 AA; 16320 MW; 69173444C679082 CRC64;
CC -----
Query Match 28.7%; Score 207; DB 1; Length 146;
Best Local Similarity 42.5%; Pred. No. 1.5e-14;
Matches 37; Conservative 16; Mismatches 32; Indels 2; Gaps 2;
QY 42 TFLAKKPGC-GLRITTDACMGRCETWEKRPLEPPYIEAHNRKCYTNETKQVTLNPCA 100
Db 41 TVANEKECRPCGLVNGTITCGSHCLT-KEPYKSPFSYVYQHVYRVRRTVRLPCP 99
QY 101 PGVDPEFTYTPVAIRCDCGACSTATTEC 127
Db 100 PGVDPHITYPVALSCDCSLCTMDTSDC 126
RESULT 7
ID GTH2_CLAGA STANDARD; PRT; 138 AA.
AC P53543;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Clarias gariepinus (Sharp-tooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Clariidae; Clarias.
OX NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=pituitary;
RA Rebers F.E.M., Tensen C.P., Schulz R.W., Goos H.J.T., Bogerd J.;
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-138.
RC TISSUE=pituitary;
RX MEDLINE=93051153; PubMed=1426937;
RA Koide Y., Noso T., Schouten G., Peute J., Zandbergen M.A., Bogerd J.,
RA Schulz R.W., Kawachi H., Goos H.J.;

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RT "Maturational gonadotropin from the African catfish, Clarias
RT gariepinus: purification, characterization, localization, and
RT biological activity."
RL Gen. Comp. Endocrinol. 87:327-341(1992).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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-----
DR EMBL; X97761; CAA66359.1; -.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Glyco_hormone_beta.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Glycoprotein; Signal.
FT CHAIN 1 21
FT SIGNAL 1 21
FT CHAIN 22 138
FT DISULFID 27 75
FT DISULFID 41 90
FT DISULFID 44 128
FT DISULFID 52 106
FT DISULFID 56 108
FT DISULFID 111 118
FT CARBOHYD 31 31
SQ SEQUENCE 138 AA; 15772 MW; 670D81FAFAC6880E CRC64;

Query Match 28.3%; Score 204; DB 1; Length 138;
Best Local Similarity 40.2%; Pred. NO.2.8e-14;
Matches 35; Conservative 18; Mismatches 32; Indels 2; Gaps 2;

QY 42 TFLAKKPGC-RGLRITTDACGRCETWEKPLEPPYIEAHHRVCTYNETQVTKLPNCA 100
DB 33 TVSEKSGCKCLAFQFISCSGHCFI-KEPVYKSPFSIYOHCTYADVETIRLPDCR 91
QY 101 PGVDPFTYTYVAIRCDGACSTATTEC 127
DB 92 PGVDPHTYTPVALSCSCSLCTMDTSDC 118

RESULT 8
LSHB_SHEEP STANDARD; PRT; 141 AA.
ID LSHB_SHEEP P01231;
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (interstitial cell stimulating hormone).
GN LHB.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93351742; PubMed=8349025;
RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
RT "Characterization of the ovine LH beta subunit gene: the promoter
RT directs gonadotroph-specific expression in transgenic mice.";
RL Mol. Cell. Endocrinol. 93:157-165(1993).

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Pituitary;
RX MEDLINE=90245669; PubMed=2336396;
RA D'Angelo-Bernard G., Mounimi M., Jutisz M., Counis R.;
RT "Cloning and sequence analysis of the cDNA for the precursor of the
RT beta subunit of ovine luteinizing hormone.";
RL Nucleic Acids Res. 18:2175-2175(1990).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=72211145; PubMed=4556309;
RA Liu W.-K., Nahm H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
RT "The primary structure of ovine luteinizing hormone. II. The amino
RT acid sequence of the reduced, S-carboxymethylated A-subunit (LH-
RT beta).";
RL J. Biol. Chem. 247:4365-4381(1972).
RN [4]
RP SEQUENCE OF 21-139.
RX MEDLINE=73190035; PubMed=4575435;
RA Sairam M.R., Samy T.S.A., Papkoff H., Li C.H.;
RT "The primary structure of ovine interstitial cell-stimulating
RT hormone. II. The beta subunit.";
RL Arch. Biochem. Biophys. 153:572-586(1972).
RN [5]
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX MEDLINE=76068152; PubMed=1201911;
RA Chung D., Sairam M.R., Li C.H.;
RT "The primary structure of ovine interstitial cell stimulating
RT hormone. IV. Disulfide bridges of the beta subunit.";
RL Int. J. Pept. Protein Res. 7:487-493(1975).
RN [6]
RP STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=91006170; PubMed=2209620;
RA Weisshaar G., Hiyyama J., Renwick A.G.C.;
RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis
RT by one- and two-dimensional 1H-NMR spectroscopy.";
RL Eur. J. Biochem. 192:741-751(1990).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
-----
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-----
DR EMBL; S64695; AAB27819.1; -.
DR EMBL; X52488; CAA36729.1; -.
DR PIR; A01500; UFSHB.
DR PIR; S09332; S09232.
DR HSSP; P01233; 1XUL.
DR GlycoSuiteDB; P01231; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Glyco_hormone_beta.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141
FT DISULFID 29 77
FT DISULFID 43 92
FT DISULFID 46 130

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FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120
FT MOD_RES 21 21
FT CARBOHYD 33 33
FT VARIANT 138 141
FT CONFLICT 30 30 Q -> E (IN REF. 4).
FT CONFLICT 59 59 L -> P (IN REF. 1).
FT CONFLICT 63 63 R -> Q (IN REF. 2).
FT CONFLICT 71 72 PM -> PPM (IN REF. 4).
FT CONFLICT 81 81 E -> Q (IN REF. 4).
FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).
FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).
SQ SEQUENCE 141 AA; 15184 MW; C59EC7C0AA55A9DC CRC64;

Query Match 28.0%; Score 202.5; DB 1; Length 141;
Best Local Similarity 39.2%; Pred. No. 4.1e-14;
Matches 47; Conservative 19; Mismatches 45; Indels 9; Gaps 5;

Oy 11 MALLLAGYGVLAGSGNLRFTVGCAYAREFFFLAKKPGCR-GLRITTDACWGRCEWKEK 69
Db 7 LLMLLLGVAGV-WASRGRPLRL--CQPLNATLAAEKKEKPCYITFTTISICAGYLSMKR 63
Oy 70 --PILEPYLEAHNRVCYTNKQVTKLPLNCAPGVDPFTYTPVALRDCGACSTATTEC 127
Db 64 VLPVILPMPQ---RVCTYHELRFASVRLPGCPGVDPKVSFPVALSCHGCRSLSTDC 120

RESULT 9
GTH2_ANGAN ID STANDARD; PRT; 140 AA.
AC P27767;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=90334705; PubMed=2116136;
RA Querat B., Mounni M., Jutisz M., Fontaine Y.A., Counis R.;
RT "Molecular cloning and sequence analysis of the cDNA for the putative
beta subunit of the type-II gonadotrophin from the European eel.";
RL J. Mol. Endocrinol. 4:257-264(1990).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.
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-----
CC EMBL: X61039; CAA43374.1; -.
CC PIR: A48166; A48166.
CC HSSP: P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR001545; Glyco_hormone_beta.
CC Pfam: PF00007; Cys_knot.1.
CC PRINTS: PR00438; GFCYSKNOT.
CC SMART: SM00068; GHB; 1.
```

```
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Signal; Hormone; Glycoprotein.
FT CHAIN 1 24 BY SIMILARITY.
FT SIGNAL 25 140 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 30 78 BY SIMILARITY.
FT DISULFID 44 93 BY SIMILARITY.
FT DISULFID 47 131 BY SIMILARITY.
FT DISULFID 55 109 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 114 121 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 140 AA; 15478 MW; 10312C061717D80 CRC64;

Query Match 27.9%; Score 201.5; DB 1; Length 140;
Best Local Similarity 38.9%; Pred. No. 5.2e-14;
Matches 42; Conservative 16; Mismatches 47; Indels 3; Gaps 3;

Oy 21 CVLGASGNLRFTVGCAYAREFFFLAKKPGC-RGLRITTDACWGRCEWKEKPILEPYIEA 79
Db 16 CHLVASAG-SLLRCEPINEIISVEKDCGCPCLVFQTSICSHCIT-KDPSYKSLSTV 73
Oy 80 HHRVCTYETKQVTKLPLNCAPGVDPFTYTPVALRDCGACSTATTEC 127
Db 74 YORVCTYDVRVETVRLPDCRGVDPHYTFVALSCDNLCTMTSDC 121

RESULT 10
GTH2_ONCKE ID STANDARD; PRT; 142 AA.
AC P10256;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1990 (Rel. 13, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90046849; PubMed=2813416;
RA Sekine S., Saito A., Itoh H., Kawauchi H.;
RT "Molecular cloning and sequence analysis of chum salmon gonadotropin
cDNAs.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8645-8649(1989).
RN [2]
RN SEQUENCE OF 24-142.
RX MEDLINE=89053031; PubMed=3192067;
RA Itoh H., Suzuki K., Kawauchi H.;
RT "The complete amino acid sequences of beta-subunits of two distinct
chum salmon GTHs.";
RL Gen. Comp. Endocrinol. 71:438-451(1988).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.
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-----
CC EMBL: M27154; AAA49409.1; -.
CC PIR: C36179; C36179.
CC HSSP: P01233; 1XUL.
CC InterPro: IPR000359; Cys_knot.
CC InterPro: IPR002400; GF_cysknot.
```

DR InterPro: IPR001545; Glyco\_hormone\_beta.  
DR Pfam: PF00007; Cys\_knot; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR SMART: SM00068; GHb: 1.  
DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
DR Hormone; Glycoprotein; Signal.  
FT SIGNAL 1 23  
FT CHAIN 29 142 GONADOTROPIN BETA-II CHAIN.  
FT DISULFID 24 77 BY SIMILARITY.  
FT DISULFID 43 92 BY SIMILARITY.  
FT DISULFID 46 130 BY SIMILARITY.  
FT DISULFID 54 108 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 113 120 BY SIMILARITY.  
FT CARBOHYD 33 73 N-LINKED (GLCNAC. . .).  
FT VARIANT 73 73 Y -> I.  
FT VARIANT 86 86 T -> K.  
SQ SEQUENCE 142 AA; 15672 MW; E31E117DA235C486 CRC64;

Query Match 27.8%; Score 201; DB 1; Length 142;  
Best Local Similarity 34.7%; Pred. No. 5.9e-14;  
Matches 42; Conservative 19; Mismatches 44; Indels 16; Gaps 3;

QY 22 VLGASSGNLFRTFGCAVRE-----FTFLAKKPGC-RGLRTTDACMGRCET 66  
DB 1 MLGHLVGLILFLCILEPVEGSLMOPCOPINOTVSLKKGCCPTCLVITPTISGHCVT 60  
QY 67 WEKPILEPPYIAHHRCVCTNETKQVTKLPNCAGVDPFYTPVAIRCDGACSTATTE 126  
DB 61 -KEPVFSPSTVYOHCTYDVRETRILPDCPPWDPHTYTPVALSCDCLCMPTSD 119

OY 127 C 127  
DB 120 C 120

RESULT 11  
GTHB\_FUHHF  
ID GTHB\_FUHHF STANDARD; PRT; 136 AA.  
AC P30972;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Gonadotropin beta-II chain precursor (GTH-II-beta).  
OS Fundulus heteroclitus (Killifish) (Mummichog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Fundulidae; Fundulus.  
OX NCBI\_Taxid=8078;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary;  
RX MEDLINE=92405806; PubMed=1526312;  
RA Lin Y.-W.P., Ruppow B.A., Price D.A., Greenberg R.M., Wallace R.A.;  
RT "Fundulus heteroclitus gonadotropins. 3. Cloning and sequencing of  
gonadotropic hormone (GTH) I and II beta-subunits using the  
polymerase chain reaction.";  
RL Mol. Cell. Endocrinol. 85:127-139(1992).  
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
FAMILY.

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CC -----  
DR EMBL: M87015; AAB59963.1; -  
DR HSSP: P01233; IXUL.  
DR InterPro: IPR000359; Cys\_knot.  
DR InterPro: IPR002400; GF\_cyskn.  
DR InterPro: IPR001545; Glyco\_hormone\_beta.  
DR Pfam: PF00007; Cys\_knot; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR SMART: SM00068; GHb: 1.  
DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
DR Hormone; Hormone; Glycoprotein.  
FT SIGNAL 1 21  
FT CHAIN 22 136 GONADOTROPIN BETA-II CHAIN.  
FT DISULFID 27 75 BY SIMILARITY.  
FT DISULFID 41 90 BY SIMILARITY.  
FT DISULFID 44 128 BY SIMILARITY.  
FT DISULFID 52 106 BY SIMILARITY.  
FT DISULFID 56 108 BY SIMILARITY.  
FT DISULFID 111 118 BY SIMILARITY.  
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 136 AA; 15016 MW; 716576844A6A1653 CRC64;

Query Match 27.6%; Score 199; DB 1; Length 136;  
Best Local Similarity 41.9%; Pred. No. 9.1e-14;  
Matches 39; Conservative 12; Mismatches 40; Indels 2; Gaps 2;

QY 36 CAVREFTFLAKKPGCRGL-RITTDACMGRCETWEKPILEPPYIAHHRCVCTNETKQV 94  
DB 27 COLNLQNTLSLEKRCGSGCHRVETITGSGCAT-KDPNFKTSYKNAIGVCTYGDLYKTF 85  
QY 95 KLPNCAAGVDPFYTPVAIRCDGACSTATTEC 127  
DB 86 EEPCEVPGVDPVTPYTPVALSCGCGCAMATSDC 118

RESULT 12  
GTHB\_MURCI  
ID GTHB\_MURCI STANDARD; PRT; 113 AA.  
AC P12837;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Gonadotropin beta chain.  
OS Muranesox cinereus (Pike eel) (Daggeetooth pike conger).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Congroidei;  
OC Muranesocidae; Muranesox.  
OX NCBI\_Taxid=7946;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pituitary;  
RX MEDLINE=90092087; PubMed=2598923;  
RA Liu C.-S., Huang F.-L., Chang Y.-S., Lo T.-B.;  
RT "Pike eel (Muranesox cinereus) gonadotropin. Amino acid sequences of  
both alpha and beta subunits.";  
RL Eur. J. Biochem. 186:105-114(1989).  
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
FAMILY.

CC PIR: S07092; S07092.  
DR HSSP: P01233; IXUL.  
DR InterPro: IPR000359; Cys\_knot.  
DR InterPro: IPR002400; GF\_cyskn.  
DR InterPro: IPR001545; Glyco\_hormone\_beta.  
DR Pfam: PF00007; Cys\_knot; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR SMART: SM00068; GHb: 1.  
DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
KW Hormone; Glycoprotein.

FT	DISULFID	6	54	BY SIMILARITY.
FT	DISULFID	20	69	BY SIMILARITY.
FT	DISULFID	23	107	BY SIMILARITY.
FT	DISULFID	31	85	BY SIMILARITY.
FT	DISULFID	35	87	BY SIMILARITY.
FT	DISULFID	90	97	BY SIMILARITY.
FT	CARBOHYD	10	10	N-LINKED (GLCNAC. . .).
SO	SEQUENCE	113 AA;	12582 MW;	1/DDGDAD6AC6A657 CRR64;

Query Match	27.48;	Score 198;	DB 1;	Length 113;
Best Local Similarity	-42.58;	Pred. No. 9.6e-14;		
Matches 37; Conservative	14;	Mismatches 34;	Indels 2;	Gaps 2;

QY TELAAKPPC-GGLRTTDTACMGRETEWKP<sup>1</sup>PLEPPT<sup>2</sup>EAHNHRTVEY<sup>3</sup>NETKOV<sup>4</sup>EVK<sup>5</sup>LPENCA<sup>6</sup> 100

42 TELAAKPPC-GGLRTTDTACMGRETEWKP<sup>1</sup>PLEPPT<sup>2</sup>EAHNHRTVEY<sup>3</sup>NETKOV<sup>4</sup>EVK<sup>5</sup>LPENCA<sup>6</sup> 100

Db TISVKKDCGRCPLVQFQISIGSGHCIT-KDPSYKSP<sup>1</sup>PLSTVVGROVCTYADNREY<sup>2</sup>RLPDCR<sup>3</sup> 70

12 TISVKKDCGRCPLVQFQISIGSGHCIT-KDPSYKSP<sup>1</sup>PLSTVVGROVCTYADNREY<sup>2</sup>RLPDCR<sup>3</sup> 70

QY PGVDPPFTYTPVAIRKDCGACGASTATTEC 127

101 PGVDPPFTYTPVAIRKDCGACGASTATTEC 127

Db PGVDPPHTEFPVALSDCNCILMTMDISDC 97

71 PGVDPPHTEFPVALSDCNCILMTMDISDC 97

RESULT	13	
GT_H2_THUOB		
ID	GT_H2_THUOB	STANDARD;
		PRT; 115 AA.

DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Gonadotropin beta-II chain (GTH-II-beta).  
DS *Thunnus obesus* (Bigeye tuna).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neuteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; Thunnus.  
NCBI\_TaxID=8241;

RC TISSUE=pituitary; PubMed=8138353;  
RX MEDLINE=94186287;  
RA Okada T., Kawazoe I., Kimura S., Sasamoto Y., Aida K., Kanauchi H.;  
RT "Purification and characterization of gonadotropin I and II from  
pituitary glands of tuna (*Thunnus ocellatus*).";  
RT Int. J. Pept. Protein Res. 43:65-80(1994).  
CC -1- FUNCTION: INVOLVED IN GONADOTROGENESIS AND STEROIDOGENESIS.  
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN

DR HSBP; P01433; 1AOL. Cys\_knot.  
DR InterPro: IPR000359; Cys\_knot.  
DR InterPro: IPR002400; GF\_cysknott.  
DR InterPro: IPR001545; Glyco\_hormone\_beta.  
DR Pfam: PF000007; Cys\_knott; 1.  
DR PRINTS: PR00438; GFCSYKNOT.  
DR SMART: SM00041; CT; 1.  
DR SMART: SM00068; GHb; 1.  
DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
KW Hormone; Glycoprotein.  
FT DISULFID 6 54 BY SIMILARITY.  
FT DISULFID 20 69 BY SIMILARITY.  
FT DISULFID 23 107 BY SIMILARITY.  
FT DISULFID 31 85 BY SIMILARITY.  
FT DISULFID 35 87 BY SIMILARITY.  
FT DISULFID 50 97 BY SIMILARITY.  
FT CARBOHD 10 10 N-LINKED (GLCNAC...).  
SQ SEQUENCE 115 AA: 12992 MW: 872107836F5C8E9 CRC64;

Query Match	27.3%;	Score 197;	DB 1;	Length 115;
Best Local Similarity	38.7%;	Pred. No. 1.2e-13;		
Matches	36;	Conservative 17;	Mismatches 38;	Indels 2;
				Gaps 2

[illegible]

RESULT	14
FSHB_RANCA	
ID_FSHB_RANCA	STANDARD;
	PRT; 107 AA

DT 16-OCT-2001 (rel. 40, created)  
DT 16-OCT-2001 (rel. 40, last sequence update)  
DT 16-OCT-2001 (rel. 40, last annotation update)  
DE Follicle-stimulating hormone beta subunit)  
DE (FSH-beta) (FSH-B).  
GN FSHB.  
OS *Rana catesbeiana* (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranolidae; Ranidae; Rana  
NCBI\_TaxID=8400;

RP SEQUENCE.  
RX MEDLINE=93051178; PubMed=1426958;  
RA Hayashi T., Hanaoka Y., Hayashi H.;  
RT "The complete amino acid sequence of the follitropin beta-subunit of  
Rt the bullfrog, *Rana catesbeiana*."  
RL Gen. Comp. Endocrinol. 88:144-150(1992).  
CC -I- FUNCTION: STIMULATES DEVELOPMENT OF FOLLICLE AND SPERMATOGENESIS  
CC IN THE REPRODUCTIVE ORGANS.  
CC  
CC -I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC -I- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN  
CC FAMILY.

DR	InterPro; IPRO00359; Cys_knot.			
DR	InterPro; IPR001545; Glyco_hormone_beta.			
DR	Pfam; PF00007; Cys_knot. 1.			
DR	SMART; SM00068; GHb. 1.			
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.			
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.			
KW	Hormone; Glycoprotein.	49		
FT	DISULFID	1		BY SIMILARITY.
FT	DISULFID	15	64	BY SIMILARITY.
FT	DISULFID	18	102	BY SIMILARITY.
FT	DISULFID	26	80	BY SIMILARITY.
FT	DISULFID	30	82	BY SIMILARITY.
FT	DISULFID	85	92	BY SIMILARITY.
FT	CARBOHYD	5	5	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. . .).
SQ	SEQUENCE	107 AA; 11794 MW; 64736a6bE1B077EC	CRC64	

Query Match	27.1%	Score 196;	DB 1;	Length 107;
Best Local Similarity	41.5%;	Pred. No. 1.5e-13;		
Matches 39;	Conservative 14;	Mismatches 37;	Indels 4;	Gaps 3;

QY	36	CANDEPFLAKKOGGSLRTTIDAC--	ORCSTMEKRLERUENHNHSTENKOU	92
QY	1	CELSNTITVTEKEEC--GACYSVNATKCS	STYCTKANKIMFYKSE--KQGVSTTEUYLET	56
Db				
QY	94	WLPNCAPGVDPFYTYYPVALRCDCG	AGCATSTATTEC	127
Db				
QY	59	WKIGCAENNNPETYYPVAVDCHCGK	CSSETTDC	92

RESULT	15	
GTH2_ONCMA		
ID	GTH2_ONCMA	STANDARD;
		PRT;
		142 AA



Search completed: July 9, 2002, 13:37:35.  
 Job time: 210 sec

```

AC P48253;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gonadotropin beta-II chain precursor (GTH-II-beta).
OS Oncorhynchus masou (Cherry salmon) (Masu salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8020;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=94197893; Pubmed=8148035;
RA Kato Y., Gen K., Maruyama O., Tomizawa K., Kato T.;
RT "Molecular cloning of cDNAs encoding two gonadotrophin beta subunits
RT (GTH-I beta and -II beta) from the masu salmon, Oncorhynchus masou:
RT rapid divergence of the GTH-I beta gene."
RL J. Mol. Endocrinol. 11:275-282(1993).
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC -----
DR EMBL: S69276; AAB30424.1; -.
DR HSSP: P01233; 1XUL.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001545; Glyco_hormone_beta.
DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS: PRO0438; GFCYSKNOT.
DR SMART: SM00068; GHB; 1.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 142 GONADOTROPIN BETA-II CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC ...) (POTENTIAL).
SQ SEQUENCE 142 AA; 15684 MM; 70A3906EAB3FF6 CRC64;

Query Match 26.6%; Score 192; DB 1; Length 142;
Best Local Similarity 33.9%; Pred. No. 5e-13;
Matches 41; Conservative 18; Mismatches 46; Indels 16; Gaps 3;

OY 22 VLASSGNLRTFGCAVRE-----FTFLAKKPGC-RGLRITTDACWGRCE 66
DB 1 MGLGHVGLISLILCEPLEPEVSGSLMOPCPINOTVSLKEGCPCLVITPTICSGHCIT 60
OY 67 WEKPILEPPYLEAHHRCTVNETKOVYKILPCAPGVDPFTYPAVIRCDGACSTATTE 126
DB 61 -KEPVFNSPFSTVYQHCTYDRVREIRLPDCPPWVDHVTYPAVASCDCSLCNDTSD 119
OY 127 C 127
DB 120 C 120
  
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 9, 2002, 13:33:25 ; Search time 27.1 Seconds  
(without alignments)  
829.865 Million cell updates/sec

Title: US-09-723-970-1  
Perfect score: 722  
Sequence: 1 MKIAFLFLGPMALLLAGYG.....VAIRDCGACSTATTECETI 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvirus:\*  
17: sp\_bacteriap:\*  
sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	29.2	128	13	091997
2	208	28.8	140	13	098173
3	205.5	28.5	123	13	0904K1
4	204.5	28.3	142	13	090D92
5	201.5	27.9	137	13	090WC1
6	201	27.8	140	13	090D80
7	195	27.0	145	13	090W55
8	194.5	26.9	146	13	090W19
9	192.5	26.7	131	13	090W63
10	191.5	26.5	145	13	090WD2
11	189	26.2	137	13	091999
12	189	26.2	146	13	090DEH0
13	188	26.0	138	13	090WC9
14	186.5	25.8	88	13	090W07
15	180	24.9	135	11	0924A7
16	180	24.9	141	11	0924A8

17	179	24.8	121	13	090W64	090W64 scyllorhinu
18	178	24.7	139	11	062778	062778 rattus norv
19	175	24.2	127	11	0924A6	0924A6 cavia porce
20	174	24.1	165	6	09BEH2	09BEH2 macaca fasc
21	173.5	24.0	142	6	09BD19	09BD19 panthera tl
22	168.5	23.3	132	13	090D81	090D81 ictalurus p
23	167.5	23.2	141	6	095J85	095J85 monodelphis
24	165	22.9	129	6	095J82	095J82 monodelphis
25	164	22.7	165	6	09BEH1	09BEH1 macaca fasc
26	161	22.3	129	6	09BD10	09BD10 panthera tl
27	160	22.2	150	13	013051	013051 cyprinus ca
28	159	22.0	147	13	013052	013052 ctenopharyn
29	159	22.0	150	13	09PW21	09PW21 aristichthy
30	158	21.9	125	13	091992	091992 conger cong
31	157	21.7	109	13	091998	091998 acipenser b
32	154.5	21.4	138	4	016163	016163 homo sapien
33	154	21.3	89	6	046618	046618 equus zebra
34	154	21.3	89	6	046619	046619 equus hemio
35	149.5	20.7	82	6	046622	046622 ceratotheri
36	149	20.6	123	13	09W608	09W608 salmo salar
37	148	20.5	130	13	098RY2	098RY2 myliopharyng
38	145	20.1	165	6	09GL37	09GL37 macaca mula
39	145	20.1	165	11	099P48	099P48 mus musculu
40	144	19.9	138	6	095J88	095J88 monodelphis
41	144	19.9	149	13	09PW9	09PW9 carassius a
42	144	19.9	150	13	013049	013049 carassius a
43	143.5	19.9	137	13	09D693	09D693 oncorhynch
44	137.5	19.0	80	11	063013	063013 rattus norv
45	134.5	18.6	130	13	091IB3	091IB3 carassius a

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	128 AA.
ID	091997	091997		
AC	091997	091997		
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	FOLLICLE-STIMULATING HORMONE PRECURSOR.			
GN	FSH.			
OS	Acipenser baerii (Siberian sturgeon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;			
OC	Acipenserinae; Acipenser.			
OX	NCBI_TaxID=27689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PIUTARY;			
RX	MEDLINE=20318422; PubMed=10859263;			
RA	Querat B., Sellouk A., Salmon C.;			
RT	*Phylogenetic analysis of the vertebrate glycoprotein hormone family including new sequences of sturgeon (Acipenser baerii) subunits of the two gonadotropins and the thyroid stimulating hormone *;			
RT	two gonadotropins and the thyroid stimulating hormone *;			
RL	Biol. Reprod. 63:232-238(2000).			
DR	EMBL; AJ251658; CAB83504.1; -.			
DR	HSSP; P01233; 1XU.			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Glyco_hormone_beta.			
DR	Pfam; PF00007; Cys_knot; 1.			
DR	SMART; SM00068; GHB; 1.			
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
FT	SEQUENCE			

Query Match 29.28; Score 211; DB 13; Length 128;  
Best Local Similarity 42.7%; Pred. No. 1,7e-16;  
Matches 41; Conservative 15; Mismatches 38; Indels 2; Gaps 2;

Oy		36	CABVEEFLEFLAKKGGCGG-TRITDAGCMGCETMEKPILEPPIEAHHNCTYMETQVNV	98
Dd		22	CALNNITIGTEKKGGCNGCVSVNTISAGCCLT-QADVYKSSISLYTLVCTFEISIVY	80
Oy		95	KLPNCARGVDPEFTYVPVAIRKDCGACSTATTECEPTI	130
Dd		81	QLPNCPEHVDPEFTYVPVALSCGEGCATDYDDCGLT	116
RESULT		2		
O98TY3	PRELIMINARY;	PRT;	140 AA.	
ID	O98TY3			
AC	O98TY3:			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	LUTEINIZING HORMONE BETA SUBUNIT.			
OC	Mylolpharyngodon pliceus.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;			
OC	Cypriniformes; Cyprinidae; Mylolpharyngodon.			
OX	NCBI_TaxID=75356;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bayer-Eisenberg D., Rosenfeld H., Zmora N., Yaron Z., Elizur A.;			
RL	"Isolation and characterization of the black carp lh beta subunit.",			
RL	Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF319960; AAK07414.1; -.			
DR	HSSP; P01233; 1XU.			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Glyco_hormone_beta.			
DR	Pfam; PF00007; Cys_knot; 1.			
DR	SMART; SM00068; GHF; 1.			
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.			
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.			
SQ	SEQUENCE 140 AA: 15820 MW: 8f12723f35d5a010 CRC64;			
Query Match		28.8%; Score 208; DB 13; Length 140;		
Best Local Similarity		37.9%; Pred. No. 4e-16;		
Matches	44; Conservative	19; Mismatches	49; Indels	4; Gaps
Oy		13	LLLAGGVGLGASSGNLRTFVSCAVREFTPLAKRPGC-RGIRITTDACMGRCETMEKPI	71
Dd		8	LLLFLCYVLVLVFAQSFF--LPPCEPVNNTVAVEKEGCPKCLVLOTITCSHCILT-KEY	64
Oy		72	LEPPIEAHHNCTYNETKOVTVKLPLNCARGVDPEFTYVPVAIRKDCGACSTATTEC	127
Dd		65	YKSPFSYVGHCVTYRDVRYEVRFLPDCCPGVDPHITYVPVALSCDSICSTWIDSDC	120
RESULT		3		
O90ZK1	PRELIMINARY;	PRT;	123 AA.	
ID	O90ZK1			
AC	O90ZK1:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	FOLLICLE STIMULATING HORMONE BETA SUBUNIT PRECURSOR			
DE	(FRAGMENT).			
OS	Rana ridibunda (Laughing frog) (Marsh frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;			
OX	NCBI_TaxID=8406;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PITUITARY;			
RA	Querat B.;			
RL	"Evolution of glycoprotein hormones in gnathostomes.";			
RL	Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.			
EMBL; AJ311356; CAC39253.1; -.				
KM	Signal.			

FT	NON TER	1	1	POTENTIAL.
FT	SIGNAL	<1	16	
FT	CHAIN	17	123	POLITICE STIMULATING HORMONE BETA
FT	SEQUENCE	123 AA;	13678 MW;	SUBUNIT
SO	SEQUENCE	123 AA;	13678 MW;	926C3E72EECCA85 CRC64;
Query Match				
Best Local Similarity		28.5%; Score 205.5; DB 13; Length 123;		
Matches		45; Conservative 15; Mismatches 44; Indels 7; Gaps 4;		
OY	19	YGVVLGASSGNLRTFVGCAVREFFLAKKPGCGRLRITTDACW--GCEIWEKPILEPPY	76	
DB	3	YGLVY---FWNMLSATCELSNITIVLEKEEC-GACISVNAWCGCYCYTMDPNLMYRQK	58	
OY	77	IEAHNRVCQYNETKQVTKLRPNCAGVDPPEFYPAIRGDCGACSTATTEC	127	
DB	59	SE-KQGVCTYEIVYETVAKIPGCADUNNPEFYPAVADHDCGRCSSETTDC	108	
RESULT 4				
ID	O9DG92	PRELIMINARY;	PRT;	142 AA.
AC	O9DG92;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	LUTENIZING HORMONE BETA SUBUNIT.			
GN	LH BETA.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Morita T., Yoshizaki G., Takeuchi T.:			
RT	"Rainbow trout lutelizing hormone beta subunit mRNA.";			
RL	submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB050836; BAB17687.1; -			
DR	HSSP; P01233; 1XU.			
DR	InterPro; IPR000359; Cys_knot.			
DR	InterPro; IPR001545; Glyco_hormone_beta.			
DR	Pfam; PF00007; Cys_knot; 1.			
DR	SMART; SM00068; GHb; 1.			
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.			
SO	SEQUENCE	142 AA;	15824 MW;	7C399C4FB1FAE55A CRC64;
Query Match				
Best Local Similarity		28.3%; Score 204.5; DB 13; Length 142;		
Matches		46; Conservative 20; Mismatches 49; Indels 9; Gaps 5;		
OY	6	LFLGPMALLLGGYGV-LGASSGNLRTFVGCAVREFFLAKKPGC-RGLRITTDACMGR	63	
DB	4	LHVGILLISLL-----CILLEPEVGSLL-MQCPQPINQIYSVKECGPCIVLTQITCSGH	57	
OY	64	CETWEKPILEPPYIEAHNRVCQYNETKQVTKLRPNCAGVDPPEFYPAIRGDCGACST	123	
DB	58	CVT-KEPVKSPFSFYVQNVCTYRDVRETIRLRPCRPVMDHNVYPAVALSCDCLCNMD	116	
OY	124	TTEC	127	
DB	117	TSDC	120	
RESULT 5				
ID	O90WC1	PRELIMINARY;	PRT;	137 AA.
AC	O90WC1;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		

DE LUTROPIN BETA SUBUNIT.  
OC Xenopus laevis (African clawed frog).  
OC Euryarchaea: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PIUTARY;  
RX MEDLINE=21309951; PubMed=11404476;  
RA Huang H., Cai L., Remo B.F., Brown D.D.;  
RT "Timing of metamorphosis and the onset of the negative feedback loop  
RT between the thyroid gland and the pituitary is controlled by type II  
RT iodothyronine deiodinase in Xenopus laevis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7348-7353(2001).  
DR EMBL: AF360397; AAK49986.1;  
SQ SEQUENCE 137 AA; 15272 MW; 6B215F1200F0E197 CRC64;  
  
Query Match 27.9%; Score 201.5; DB 13; Length 137;  
Best Local Similarity 35.8%; Pred. No. 2.2e-15;  
Matches 44; Conservative 16; Mismatches 54; Indels 9; Gaps 4;  
  
OY 6 LFLGPMALLLAGVCVIGASSGNLRITVGCAREFTFLAKKPGCR-GLRITTDACWGRG 64  
DB 1 MERSQVTLFLIGFY---LSAVOGRRL---CHPTNATISAERKDCPCIVTLTTVCTGCG 53  
OY 65 EFWEXPILEPIEHHVHCYNETKQYTVKLPNCAPGVDPFYTYPVAINRDCGACSTAT 124  
DB 54 LTRDPVKMALSSVYQNICYNETRIYDTIKLPDCLPGTDPFTYPAVAVSCCKNCKMDY 112  
OY 125 TEC 127  
DB 113 SDC 115  
  
RESULT 6  
O9DGB0 PRELIMINARY; PRT; 140 AA.  
AC O9DGB0:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GONADOTROPIN BETA 2 SUBUNIT.  
OS Ictalurus punctatus (Channel catfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Siluriformes; Ictaluridae; Ictalurus.  
OX NCBI\_TaxID=7998;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KANSAS;  
RA Liu Z.-J., Kim S., Karsi A., Dunham R.;  
RT "Channel catfish gonadotropin beta-subunits: cDNA cloning and their  
RT expression during ovulation."  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF112192; AAG32156.1;  
DR HSSP: P01233; 1XUL;  
DR InterPro: IPR000359; Cys\_knot.  
DR InterPro: IPR001545; Glyco\_hormone\_beta.  
DR Pfam: PF00007; Cys\_knot; 1.  
DR SMART: SM00068; GHb; 1.  
DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA.1; UNKNOWN.1.  
SQ SEQUENCE 140 AA; 15787 MW; AAA74CAATFE3D2882 CRC64;  
  
Query Match 27.8%; Score 201; DB 13; Length 140;  
Best Local Similarity 36.1%; Pred. No. 2.5e-15;  
Matches 43; Conservative 22; Mismatches 46; Indels 8; Gaps 4;  
  
OY 12 ALLLAGVCVIGASSGNLRITV--GCAVREFTFLAKKPGC-RGIRITTDACWGRCEWE 68  
DB 7 SFLLL-----CFLMNSFPAQSAYILPHCEPVNETVSEKDGCPKCLVPQTATCSGHLN-K 61

OY 69 KPILEPIEAAHRYCTYNETKQYTVKLPNCAPGVDPFYTYPVAINRDCGACSTATTEC 127  
DB 62 EPVKKSPSNIYQHVCTRVDRYEFVRLPDCRPGDPVHTYPAVLSGCTCTCTMDTSDC 120  
  
RESULT 7  
O90W55 PRELIMINARY; PRT; 145 AA.  
AC O90W55:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE GONADOTROPIN (GTH-II) BETA SUBUNIT.  
GN GTH-II BETA.  
OS Paralichthys olivaceus (Flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Paralichthyidae; Paralichthys.  
OX NCBI\_TaxID=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PIUTARY;  
RX MEDLINE=21216564; PubMed=11316417;  
RA Kajimura S., Yoshida Y., Suzuki M., Aida K.;  
RT "cDNA cloning of two gonadotropin beta subunits (GTH-Ibeta and  
RT -Iibeta) and their expression profiles during gametogenesis in the  
RT Japanese flounder (Paralichthys olivaceus).";  
RL Gen. Comp. Endocrinol. 122:117-129(2001).  
DR EMBL: AB042423; BAB47388.1;  
SQ SEQUENCE 145 AA; 16295 MW; 8BDC5E2EB3E750CC CRC64;  
  
Query Match 27.0%; Score 195; DB 13; Length 145;  
Best Local Similarity 38.7%; Pred. No. 1.3e-14;  
Matches 36; Conservative 18; Mismatches 37; Indels 2; Gaps 2;  
  
OY 36 CAVREFTFLAKKPGC-RGLRITTDACWGRCEWEPILEPIEAAHRYCTYNETKQYTV 94  
DB 36 CLINQTVSLKEGCPKHVETITSGCHKT-KDPVAKIPPLMYQHCVYQELYYKTF 94  
OY 95 KLPNCAPGVDPFYTYPVAINRDCGACSTATTEC 127  
DB 95 ELDPDPPGVDPFYTYPVAVSCYCGKCALNTSDC 127  
  
RESULT 8  
O90W19 PRELIMINARY; PRT; 146 AA.  
AC O90W19:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LH-BETA PROTEIN PRECURSOR.  
GN LH-BETA.  
OS Hippoglossus hippoglossus (Atlantic halibut).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Pleuronectidae; Hippoglossus.  
OX NCBI\_TaxID=8267;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Weitzien F.A., Kobayashi T., Andersson E., Norberg B., Andersen O.;  
RT "Molecular characterization of FSH-beta, LH-beta, and alpha-subunit of  
RT Atlantic halibut (Hippoglossus hippoglossus).";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ417769; CAD10502.1;  
KW Signal.  
FT SIGNAL 1 31  
FT CHAIN 32 146 LH-BETA SUBUNIT.  
SQ SEQUENCE 146 AA; 16519 MW; 36C1FA04E0EF7C23 CRC64;



Query Match	26.2%	Score 189;	DB 13;	Length 146;
Best Local Similarity	39.8%	Pred. No. 6.3e-14;		
Matches	37;	Conservative 15;	Mismatches 37;	Indels 4;
				Gaps 3;

  

QY	36	CAYRFETFLAKKPGCGRLR-ITTDACMGRCEEMWERPILEPPIEAMHRYCTYINERKQTVY	94
	39	COLINQIYLSLEEGGGKCPHVPETITCSGCHIT-KPVMKTRIVYOH--VCTYRDLHYKTE	95
DB			
QY	95	KLPNCAGVDPPEYTVVAIRCDGCGASTATEEC	127
QY	96	ELPDDCPGVDEPTVYVPAVNSCHGICGACADTSTGC	128

	Query Match	26.0%	Score 188;	DB 13;	Length 138;
	Best Local Similarity	35.3%;	Pred. No. 7.8e-14;		
	Matches	41; Conservative 16;	Indels 10;	Gaps 3;	
OY	13 LLLAGGYCVLGASSGNRTFVGCAVREFTPLAKPGCR-GIRITTTDAMGRCETWEKPI 71				
	:         :				

[illegible]

	Query Match	25.8%	Score 186.5	DB 13	Length 88
	Best Local Similarity	41.2%	Pred. No. 7.2e-14		
Matches	Conservative	15	Mismatches	29	Indels
				Gaps	2
OY	48	PGCRRLRTTDAACMRCEIWEKLEPPRIEKNHNVCTNENKOYTVKIPNCAPGVDPEY	107		
Dd	2	PTC-LVIQITPICSHCVT-KEPVKSFPSTVOHVCTIRDYRFTETIRLDCPWWDDHHV	58		
OY	108	TYPVAIRCDCGACSTATTEC	127		
Dd	59	TYPVALSCDCSLCNMDTSDC	78		

RESULT	15	
0924A7		
ID	0924A7	PRELIMINARY;
AC	0924A7	PRT; 135 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	LTENINIZING HORMONE BETA SUBUNIT PRECURSOR (FRAGMENT).	
OS	Cavia porcellus (Guinea pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.	
OX	NCBI_TaxID=10141;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21255925; PubMed=11357063;	
RA	Sherman G.B., Hellman D.F., Boss A.J., Bunick D., Lund L.A.;	
RT	"Messenger RNAs encoding the beta subunits of guinea pig (Cavia	
RT	porcellus) luteinizing hormone (gplh) and putative chorionic	

RT gonadotropin (gpCG) are transcribed from a single-copy gplH/Cgbeta  
RT gene.";  
RL J. Mol. Endocrinol. 26:267-280(2001).  
DR EMBL: AF356595; AAK84306.1; -.  
KW Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 14 POTENTIAL.  
FT CHAIN 15 135 LUTEINIZING HORMONE BETA SUBUNIT.  
SQ SEQUENCE 135 AA; 14432 MW; A44C63BDC5607AE CRC64;

Query Match 24.9%; Score 180; DB 11; Length 135;  
Best Local Similarity 35.4%; Pred. No. 6.3e-13;  
Matches 46; Conservative 19; Mismatches 41; Indels 24; Gaps 7;

OY 6 LFLGPMALLLAGYGCVLGASSGNLRTFVGCAREFTFLAKKPGCR-GLRITTDACWGRC 64  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 1 LLLG-----LLSTSG--VWASRGPLRPY--CRPINATLAERKACPCVFTTSTICAGYC 52  
OY 65 -----ETWERPILEPPYIEAHHRVCYNETKQVTKLPNCAPGVDPPEYTPVAIRDC 117  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 53 PSMMEVLTARRPV---PQL-----VCTYDELRFASIRLPGCPGVDPVVSFPVALSCHC 104  
OY 118 GACSTATTTC 127  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 105 GTCRLSNSDC 114

Search completed: July 9, 2002, 13:37:17  
Job time: 232 sec